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SEARCH REQUEST FORM

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Scientific and Technical Information Center

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Requester's Full Name: Daud Fox	Examiner #: 65401 Date: $5/4/03$
A + Unit: 1/0 38 Phone Number 306 - 02-80	Serial Number: 09/940,550
Mail Box and Bldg/Room Location: 41 9 7 Resu	Its Format Preferred (circle): PAPER DISK E-MAIL
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Progre than one search is submitted, please prioritiz	e searches in order or need.
Please provide a detailed statement of the search topic, and describe a	is specifically as possible the subject matter to be searched.
Include the elected species or structures, keywords, synonyms, acrony utility of the invention. Define any terms that may have a special me	yms, and registry numbers, and combine with the concept or
known. Please attach a copy of the cover sheet, pertinent claims, and	abetract POINT OF CONTEST.
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Title of Invention:	70 CM1 6A04 703-308-2527
Inventors (please provide full names):	703-308-55
Earliest Priority Filing Date: 600	
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Online Time: Other	Other (specify)
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 "Total number of hits satisfying chosen parameters: Title: Perfect score: Run on: Database : Searched: Scoring table: Sequence: OM nucleic - nucleic search, using sw model IDENTITY_NUC
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Submitted (04-JUN-1991) S.A. Kul
Corporate Center, Indianapolis,
2 (bases 1 to 2200)
                                                                                                                                                                                                                                                                                                     Bacteriophage phiC31 ORF X59938
                                                                                                                            Kuhstoss,S. and Rao,R.N.
Analysis of the integration function of bacteriophage phi C31
J. Mol. Biol. 222 (4), 897-908 (1991)
                                                                                                                                                                                                                                               integrase; orf 613; p68
Bacteriophage phi-C31.
Bacteriophage phi-C31.
Tiruses; dsbnA viruses,
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/rpt_type=INVERTED
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SRLKVNDAIPIVSELLALGVTIVSTQEEVFRQCNVNDLIHLINKLDASHKESSIKSAK
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SSAWDPATVMRILRDPRIAGFAAEVIYKKKPDCTPTTKIEGYRIQRDPTTLREPVELDC
GPIIEPAEWYELQAWLDGRGRGKGLSRCQAILSAMDKLYCECGAVMTSKRGEESIKDS
YRCRRRKVVDPSAPGQHEGTCNVSMAALDKFVAERIENKIRHAEGDEETLALLWEAAR
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LRQQGAEERLAELEAAEAPKLPLDQWFPEDADADPTGPKSWWGRASVDDKRVFVGLFV
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alpha peptide; lacZa gene.
Cloning vector pSET152.
Cloning vector pSET152
artificial sequences; vectors.
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Cloning vector PSET152.
AJ414670
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Direct Submission
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Bohm,I., Mi
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Increasing the efficiency of heterologous promote
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                                                                                                                                                                                                                                                                                                           sequences V00635, J0
Location/Qualifiers
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      GGAAGGCGTCTTCCGGCAGGGAAACGTCATGGACCTGATTCACCTGATTATGCGGCTCGA
                                   GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA
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DKIVVTKSTTGRGGTPIEKRASITWAKPPTDDDEDDAQDGTEDVAA"

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99238410
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                                                                                                                                                                                                                                                   Smith, M.C., Burns, R.N., Wilson, S.E. and Gregory, M.A.
The complete genome sequence of the Streptomyces temperate phage straight phic31: evolutionary relationships to other viruses Nucleic Acids Res. 27 (10), 2145-2155 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage phi-C31 (AJ006589 AJ006589.1 GI:3947449
                                                                                                                                                         Submitted (01-JUN-1998) Smith M.C.M., Genetics, Nottingham, Queens Medical Centre, Nottingham,
                                                                                                                                                                                    Direct Submission
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Bacteriophage phi-C31
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                                      /gene="31"
145. .585
                                                                                                                                            Location/Qualifiers
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                                                                                                        UOT 11A
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            codon_start=1
                                                                           db_xref="taxon:10719"
                                                                                                                organism="Bacteriophage phi-C31"
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EETLDNLEADGF PVEAF PTNSLARMV PATQAVYDACRDGRLSHDGN PALGRHIGNAVL
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AQRSTEASFRIYRLSQFVRGASTWLPHGLWDSLAADDDPLEPGDEVVLGFDGSWKGDS
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ADAGRQQGLNPAAVSLDEYAFSKHSDLFDALTLGSAARNQPMFLIISTAGPDPDGPFA
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                                                                                                             /codon_start=1
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/transl_table=11
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EVUB4006 DNA circular SYN 03-MAY-1997 Expression vector pBSII-LUCINT firefly luciferase (LUCINT), beta-galactosidase (lacZ) and beta-lactamase (ampR) genes, complete cds and lac operon promoter sequence.
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AUTHORS
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U84006.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 5967)
Mankin,S.L., Allen,G.C.
Introduction of a Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-JAN-1997)
NC 27695-7612, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mankin, S.L., Allen, G.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expression Expression
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(bases 1 to 5967)
                                                                                                                                                                                                                            /gene="LUCINT"
3146. .3355
/gene="lacz"
3146. .3355
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="firefly luciferase"
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/product="firefly luciferase"
/protecln_id="AAB53627.1"
/db_xref="g1:2071945"
/db_xref="g1:2071945"
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APANDIYNERELLNSMNISOPTVVFVSKKGLOKILNVGKKLFIJGKIIIMDSKTDYGG
FOSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNGSGTGLPKGVALPHRTACVF
FSHARDPIFGNGIIPDTAILSVVPFHIGFGMFTTLGYLICGFRVVLMYRFEEELFLRS
LDDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEYGEAVAKRFHLF
LDDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEYGEAVAKRFHLF
                                                                                                                                                                                                                                                                                                                                                                                                                      GIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCV
RGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA
PAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTEKEIVDYVASQVTT
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                                                                                                                                                                                                                                                                                       2816.
                                                                                                                 /protein_id="AAB53629.1"
/db_xref="GI:2071947"
/translation="MAVVLORRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQ
                                                                                                                                                                                                                                                                                                                  /gene="LUCINT"
/standard_name="nopoline
                                                                                                                                                                                                                                                                                                                                                 2786.
                                                                                                                                                                                                                                                                                                                                                                         /gene=
                                                                                                                                                                                                                                                                                                                                                                                                          AKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKKGGKSKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(875. .1029,1219. .2716)
/gene="LUCINT"
/EC_number="1.13.12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="chimera plasmid (
(pLuk07, dsDNA) derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Expression vector
/db_xref="taxon:56405"
/plasmid="pLuk07"
/codon_start=1
/transl_table=11
                                                                                                                                                               /product="beta-galactosidase"
                                                                                                                                                                                                                                                                                                     /note-
                                                                                                                                                                                                                                                                                                                                                             note-"PIV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="LUCINT"
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                             'function="ampicillin
                                             ′gene="ampR"
                                                                                                        "RSLNGEWREIVNVNILLKFALNFC
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                                                                                                                                                                                                              'gene="lacz"
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AX259239
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Cestrum yellow leaf curling virus pro
Patent: WO 0173087-A 37 04-OCT-2001;
Syngenta Participations AG (CH)
                                                                                                                                                                                                                                                                                                                                       synthetic construct.
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                                                                                                                                                                                              /organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence synthetic 245 c 240 g 182 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="lac operon promoter"
1349 c 1416 g 1516 t
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/protein_id="AAB53628.1"
/db_xref="GI:2071946"
                                                                                                                                                                                                                                                                                                                             sequences.
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Pred. No. 6.6e-27;
D; Mismatches 9;
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Pred. No. 4.4e-27;
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                                                                    Hohn, T., Stavolone, L., de Haan, P.T., Cestrum yellow leaf curling virus pre Patent: WO 0173087-A 40 00-OCT-2001; Syngenta Participations AG (CH)
                                                                                                                                    synthetic construct synthetic construct
                                                                                                                                                                            Sequence 40
Ax259242
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Sequence
AX259244
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synthetic construct
artificial sequences.
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Cestrum yellow Leaf curling virus promoters
Patent: Wo 0173087-A 42 04-OCT-2001;
Syngenta Participations AG (CH)
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         /note="artificial sequence CmpS-synGFPI-nos
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/db_xref="taxon:32630"
/note="artificial sequence CmpC-synGFPI-nos
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95.8%;
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Pred. No. 7.4e-27;
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Cestrum yellow leaf curling virus promoters
Patent: WO 0173087-A 38 04-OCT-2001;
Syngenta Participations AG (CH)
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Syngenta Participations AG (CH); Un
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/note="artificial sequence GUS gene with intron"
/note="artificial sequence GUS gene with intron"
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563 GTTGATGTGCAGGTA 577
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Bennett,M., May,S. and Ramsay,N.
Method of using transactivation proteins to control gene expression in transgenic plants
Patent: US 5801027-A 2 01-SEP-1998;
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AR037156 1 GI:5955012
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Copyright (c) 1993 - 2003 Compugen Ltd
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ALIGNMENTS

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XX MO2 ABK12555; DNA encoding novel phi C31 integrase, phiC31intINT 18-JUN-2002 ABK12555 standard; DNA; (first entry) 2031

Phi C31 integrase; recombinase; transgenic; plant; agricultural food product; self-excising polynucleotide; gene; ds; phiC31intINT. Synthetic.

WO200216609-A2

27-AUG-2001; 2001WO-US26738. 28-FEB-2002.

(BADI) BASF PLANT SCI GMBH. (MCKE/) MCKERSIE B. 25-AUG-2000; 2000US-227961P.

Mankin L;

WPI; 2002-280939/32.

New self-excising polynucleotides, useful for producing transgenic

Claim

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food

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The invention describes an isolated excisable polynucleotide, which comprises a desired trait polynucleotide are recombinase polynucleotide operably linked to a promoter, all flanked by a pair of directly oriented self-excising polynucleotide is useful for producing transgenic plants, encode a gene product from the transgenic nucleic acid sequences that original genetic configuration of the genome. The polynucleotide is also is seful in methods for eliminating unwanted nucleic acids in agricultural food products and for preventing the escape of certain transgenic traits phic31intINT, created for use in the self-excising polynucleotide is phic31intINT, created for use in the self-excising polynucleotide
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AAAGAATGTAGTATATAGCAATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTT

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New self-excising polynucleotides, useful for producing transplants, removing transgenes from these plants or crops (e.g. commodities), and restricting the distribution of transgenes
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                                                                                                                                                       food products and for preventing the escape of certain transgenic traits into the environment. This sequence represents the plasmid pBPS EW051 T-DNA region used to test the self-excising DNA described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BADI ) BASF PLANT (MCKE/) MCKERSIE B.
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border represent the end of the
self-excising polynucleotide"
Score 2031;
Pred. No. 0;
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                                      AGGGGCAGGGAACGCCCATCGAGAAGCGCGCTTCGATCACGTGGGCGAAGCCGCCGACC
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RESULT 3
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ID ARK1
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XX ABK1
XX DNA
XX Phi
KW Phi
KW agri
KW gene
XX Synt
XX WO20
XX WO20
PD 28-F
XX Y5-l
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ABK12556 standard; DNA; 2031 ВÞ

18-JUN-2002 entry)

DNA encoding novel phi C31 integrase, phiC31int*INT

gene; ds; agricultural food product; self-excising po-qene; ds: phi73:i++***m Phi C31 integrase; recombinase; phiC3lint*INT. polynucleotide;

Synthetic

WO200216609-A2

28-FEB

27-AUG-2001; 2001WO-US26738

25-AUG-2000; 2000US-227961P

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Query Match
Best Local Sim
Matches 2021;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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CTCGCCCTGGGCGTGACGATTGTTTCCACTCAGGAAGGCGTCTTCCGGCAGGGAAACGTC
                                                      GACGTGTCGCGCTTCTCGCGCGCCTGAAGGTCATGGACGCGATTCCGGATTGTCTCGGAATTG
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                                          GACGTGTCGCGCTTCTCGCGCCTGAAGGTCATGGACGCGATTCCGATTGTCTCGGAATTG
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                      (ARTE-) ARTEMIS PHARM GMBH.
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                                                                                                                                                                                                                                                                                                  trapping construct; conditional mutation; unidirectional inversion; mbinase recognition sequence; RRS; disruption cassette; ction cassette; transgenic organism; expression vector pRK65; 31 integrase; C31-Int mediated inversion; ds.
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Cytomegalovirus.
Unidentified.
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New gene trapping construct capable of causing conditional mutations in genes, comprises functional DNA segment inserted in sense or antisense direction relative to gene to be trapped
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WPI; 2001-308486/32.

Example 78pp; English

standard DNA segment. One of the DNA segment (disruption cassette) is inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional orientation of the gene to be trapped. The cell comprising the gene trapping construct is useful for the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is useful for the identification and/or isolation of useful to study gene function at various developmental stages. The gene trapping construct is useful for mutationally inactivating all cellular genes. The present sequence is an expression vector pRK65. The pRK65 is used for the expression of phic31 integrase to detect C31-Int (a phic31 phage derived integrase) mediated inversion. two recombinase recognition sequences (RRSs) specific to site specific recombinase which is capable of unidirectional inversion of double standard DNA segment. One of the DNA segment (disruption cassette) is The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by lanked by specific

Sequence 5711 BP; 1329 A; 1512 C; 1616 G; 1254 T; 0 other;

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Query Match
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                                                                                                                  CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGATTCTCGACACGAAGAACCTTCA
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GATCGTTGTCACGAAGTCGACTACGGGCAGGGGGAACGCCCATCGAGAAGCGCGC
                                                                                                      GCTTCCCCTTGACCAATGGTTCCCCGAAGACGCCGACCGTGACCCGACCGGCCCTAAGTC
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standard; DNA; 3401 ВP

06-MAR-1991 (first entry

Sequence encoding phage phi C31. site specific integrating function of actimomycete

Antibiotic production; isovaleryl; spiramycin;

Page phi C31

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Best Local Similarity
Matches 1813; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence may be incorporated into a plasmid with an antibiotic blosynthetic gene (eg. isovaleryl or spyramycin) and used to transform a microorganism with site specific integration. Plasmids pKC796, pOJ243, pSKC50 and pSK51 and actimomycetes transformed by them, are specifically claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3401 BP; 660 A; 1011 C; 1135 G; 594 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of site-specific integrating function of phage OC31 - for increased prodn. of antibiotics and prodn. of hybrid antibiotics in actinomycetes
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                    GCGCGAATTGGGCGGGTACGTCGGCGGGAAGGCGCCTTACGGCTTCGAGCTTGTTTCGGA
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1952	GATCGTTGTCACGAAGTCGACTACGGGCAGGGGGCAGGGAACGCCCATCGAGAAGCGCCCC	1893	Qy
1892 2211	GTGGTGGGGGCGCGCGTCAGTAGACGACAAGCGCGTGTTCGTCGGGCTCTTCGTAGACAA	1833 2152	Qy Db
1832 2151	GCTTCCCCTTGACCAATGGTTCCCCGAAGACGCCGACGCTGACCCGACCGGCCCTAAGTC	1773 2092	ДЬ
1772 [†] 2091	GCTCCGGCAGCAAGGGGGCGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAAGCTCCGGCAAGCTCCGGCAAGCCCCGAAGCCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAACCTGAACCACAGCACAGCACAGAACAACAAGCCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAAGCCCCGAACCTGAACAACAACAACAACAACAAAAAAAA	1713 2032	Qy Db
1712 2031 .	AGGCGCGTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCTGAC	1653 1972	Qy Db
1652 1971	TGTTGCGGAGCGCCGACGCCCTGAACGCCCTTGAAGAGCTGTACGAAGACCGCGCGGC	1593 1912	Db Oy
1592 1911	CGCCCGACGCTTCGGCAAGCTCACTGAGGCGCCTGAGAAGAGGGGGGGAACGGGCGAACCT 	1533 1852	ОУ
1532 1851	CTTCAACAAGATCAGGCACGCCGAAGGCGACGAAGAGACGTTGGCGCTTCTGTGGGAAGC	1473 1792	Qy Db
1472 1791	GCACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCAT	1413 1732	Db dy
1412 1731	GATCAAGGACTCTTACCGCTGCCGTCGCCGGAAGGTGGTCGACCCGTCCGCCACCTGGGCA	1353 1672	Оу Db
1352 1671	CATGGACAAGCTGTACTGCGAGTGTGGCGCCCGTCATGACTTCGAAGCGCGGGGAAGAATC	1293 1612	Qу
1292 1611	GTGGTTGGACGGCAGGGGCGCGAGCAAGGGGCTTTCCCGGGGGCAAGCCATTCTGTCCGC	1233 1552	Оу
1232 1551	GCCGGTCGAGCTTGATTGCGGACCGATCATCGAGCCCGCTGAGTGGTATGAGCTTCAGGC	1173 1492	Оу
1172 1491	CGGCACGCCGACCAAGATTGAGGGTTACCGCATTCAGCGCGACCCGATCACGCTCCG	1113 1432	Оy
1112 · 1431	CCTTCGGGACCCGCGTATTGCGGGCCTTCGCCGCTGAGGTGATCTACAAGAAGAAGCCGGA	1053 1372	Фр
1052 1371	CGAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCGAAT	993 1312	ОУ
992 1311	CCCGGGCAGCATCACGGGGCTTTGTAAGCGCATGGACGCTGACGCCGTGCCGACCCGGGG	933 1252	Оу
932 1251	GCGTGAGATCAAGACGCACAAACACCTTCCCTTCAAGCCGGGCAGTCAAGCCGCCATTCA	873 1192	Оу
1191		1132	Db

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                                                                 The specification describes a method for identifying altered recombinases. The method comprises transforming cells with a first plasmid comprising two recombination sites and a coding sequence of interest, and a second plasmid encoding an altered recombinase; allowing recombination of the two recombination sites using the altered recombinase; screening and isolating transformed cells comprising the product of the sequence of interest; and identifying the altered recombinase. The altered recombinase is useful for site-specifically integrating a polymucleotide sequence of interest in a genome of a cell. It is also useful in genetic engineering of chromosomes of higher cells, and for the generation of transgenic cells, tissues, plants and animals.
The altered recombinase is useful for treating monogenic disorders, e.g. ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia, chronic granulomatous disease, Duchenne's muscular dystrophy, haemophilia, Fanconi's disease, sickle-cell anemia
                                                                                                                                                                                                                                                                                                      Identifying altered recombinase, involves hybridizing recombination sites in cells having specific coding sequence, transformed with altered recombinase gene, and isolating cells having product of the
                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                 sequence
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The specification describes a method for identifying altered recombinases. The method comprises transforming cells with a first plasmid comprising two recombination sites and a coding sequence of interest, and a second plasmid encoding an altered recombinase; allowing recombination of the two recombination sites using the altered recombinates; screening and isolating transformed cells comprising the product of the sequence of interest; and identifying the altered recombinase. The altered recombinase is useful for site-specifically integrating a polynucleotide sequence of interest in a genome of a cell. It is also useful in genetic engineering of chromosomes of higher cells, and for the generation of transgenic cells, tissues, plants and animals. The altered recombinase is useful for treating monogenic disorders, e.g. And deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia, chronic granulomatous disease, Duchenne's muscular dystrophy,
haemophilia, Fanconi's disease, sickle-cell anemia, Gaucher's disease, Hunter's syndrome and X-linked severe combined immunodeficiency (SCID) infectious diseases including viral anotherial infections, acquired disorders including solid tumours and haematopoietic cancers such as leukaemias and lymphomas, and other cancers. The present sequence encodes an altered recombinase of the invention.
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/product= "altered recombinase 5C1"
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Query Match Best Local Similarity Matches 1807; Conserv

Conservative

88.7%; Score 1801.6; 99.5%; Pred. No. 0; tive 0; Mismatches

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                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                CATGGACAAGCTGTACTGCGAGTGTGGCGCCATCATGACTTCGAAGCGCGGGGAAGAATC
                                                                                                                                                                                                                         CATGGACAAGCTGTGCGAGTGTGGCGCCGTCATGACTTCGAAGCGCGGGGAAGAATC
                                                                                                                                                                                                                                                                                    GCCGGTCGAGCTTGATTGCGGACCGATCATCGAGCCCGCTGAGTGGTATGAGCTTCAGGC
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RESULT 10
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The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which
                                                                                                 Novel
virus
                                                                                                                               WPI;
                                                                   Example
                                                                                                                                                                                         27-MAR-2000; 2000GB-0007427.
28-APR-2000; 2000GB-0010486.
26-JAN-2001; 2001EP-0101802.
                                                                                                                                                                                                                                                                                                                   Key
intron
                                                                                                                                                    Hohn
                                                                                                                                                                                                                                   26-MAR-2001; 2001WO-EP03408
                                                                                                                                                                      (SYGN)
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                                                                                                                                                                                                                                                                            WO200173087-A1
                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                           Solanum
                                                                                                                                                                                                                                                                                                                                                                                        Cestrum
                                                                                                                                                                                                                                                                                                                                                                         Cestrum yellow leaf curling virus; CmYLCV; trantransgenic plant; green fluorescent protein 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD19829 standard; DNA;
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                                                                                                                               2001-616524/71.
                                                                                             DNA sequence obtained from genome of Cestrum for conferring constitutive expression of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAAGACGTAG 1833
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                                                                                                                                                                                                                                                                                                                                                                                                         fluorescent protein-1, synGFP1 gene with ST-LS1 intron
                                                                                                                                                                     SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                            tuberosum
                                                                                                                                                 Stavolone L,
                                                                                        conferring
                                                                  Page
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                   66;
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
278..465
/*tag=_a
                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2023
                                                               100pp;
                                                                                                                                                                                                                                                                                           "Solanum tuberosum
                                                                                                                                                  De Haan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       912
                                                                English
                                                                                                                                                                                                                                                                                                                                                                                      virus; CmYLCV; transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВР
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                                                                                                                                                                      AG
                                                                                                                                                 Ligon
                                                                                                                                                 HT,
                                                                                                                                                                                                                                                                                             ST-LS1
                                                                                                                                        Kononova
                                                                                                                                                                                                                                                                                                                                                                              GFP1;
                                                                                                                                                                                                                                                                                            intron"
                                                                                              yellow leaf
associated c
                                (CmYLCV) novel an associated
                                                                                              of curling
                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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RESULT 11
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Best Local S
Matches .204
                                                  27-MAR-2000;
28-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                                        Chimeric
Chimeric
WPI; 2001-616524/71
                 Hohn
                                                                                     26-MAR-2001;
                                                                                                        04-OCT-2001.
                                                                                                                        W0200173087-A1
                                                                                                                                                                                     misc_feature
                                 (SYGN)
                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                          Chimeric
                                                                                                                                                           terminator
                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                           GFP1;
                                                                                                                                                                                                                                                                                  Cestrum yellow
transgenic plan
                                                                                                                                                                                                                                                                                                            Promoter-reporter
                                                                                                                                                                                                                                                                                                                                                                AAD19834 standard;
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                                                                                                                                                                                                                                                                                                                                               AAD19834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are used for creating transgenic plants expressing DNA of interest at a times and in most tissues and organs. The present DNA sequence is greer fluorescent protein-1, synGFP1 gene with ST-LS1 intron sequence. Plant optimised GFP reporter gene is used in the construction of plant
                                                                                                                                                                                                                                                                                                                                                                                                           445
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thes 204;
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                                                                                                                                                                                                                                                                                                                                                                                                         CCAAAATTTGTTGATGTGCAGGTGCAGGAGCGC
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                                 SYNGENTA PARTICIPATIONS
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               Stavolone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912 BP;
                                                                                                                                                                                                                                       Cestrum yellow leaf Agrobacterium tumefa Unidentified
                                                                                                                                                                                                                                                                                   plant;
                                                  ; 2000GB-0007427.
; 2000GB-0010486.
; 2001EP-0101802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                     2001WO-EP03408
                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                           /note= "CmYLCV (
380..1292
                                                                                                                                                                                                                                                                                         leaf curling virus; CmYLCV;
                                                                                                                                                         /note= "Corresponds
1304..1577
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 A; 245 C; 240 G; 182 T; 0 other;
                                                                                                                                                                                                                                                                                 nopaline
                                                                                                                                                                                                                                                                                                           cassette
               ۲
                                                                                                                                                                                                                                                                                                                                                                DNA;
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                De
                                                                                                                                      "Nopaline synthase (NOS) terminator"
                                                                                                                                                                                                                                                                                                                                                                 1577
                                                                                                                                                                                                                                                tumefaciens.
                Haan
                                                                                                                                                                                                                                                                                                            #3
                                                                                                                                                                                                                                                                                  synthase; NOS;
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                                                                                                                                                                                                                                                       curling
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               Ligon
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                                                                                                                                                                                           promoter fragment"
                                                                                                                                                                                                                                                      virus
                                                                                                                                                                                                                                                                                                                                                                                                           477
                                                                                                                                                                SynGFP1 gene
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               HT,
                                                                                                                                                                                                                                                                                 green
                                                                                                                                                                                                                                                                                          transcription;
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               Kononova
                                                                                                                                                                                                                                                                                fluorescent protein-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
               Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                          vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           444
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XX AAD19
XX AAD19
XX 18-DE
XX 18-DE
XX Cestr
KW Cestr
KW trans
XX GFP1;
OS Chime
OS Chime
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YT Promo
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Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Cestrum yellow.leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which are used for creating transgenic plants expressing DNA of interest at all times and in most tissues and organs. The present DNA sequence is a promoter reporter cassette which contains CmYLCV CmpC promoter fragment, green fluorescent protein-1 synGFP1 reporter gene and the Agrobacterium tumefaciens nopaline synthase (NOS) terminator. Promoter-reporter cassette is used to construct plant transformation vector.
                                                                                                                                                                                                                            GFP1;
             WO200173087-A1
                                                                                                  misc_feature
                                                                                                                                       promoter
                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                        transgenic
                                                                                                                                                                                                                                                     Cestrum yellow
                                                                                                                                                                                                                                                                          Promoter-reporter cassette #1 to construct plant transformation
                                                                                                                                                                                                                                                                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                                                               AAD19832;
                                                                                                                                                                                                                                                                                                                                                      AAD19832 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1577 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 19; Page 72-73; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel DNA sequence obtained from virus for conferring constitutive
                                                             terminator
                                                                                                                                                                                                                                                                                                                                                                                                                     825
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                                                                                                                                                                                                                                                                                                                                                                                                                 CCAAAATTTGTTGATGTGCAGGTACGCGGGTGC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTAGTAGTAATATAATATTTCAAATATTTTTTCAAAATAAAAGAATGTAGTATATAGCA
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                                                                                                                                                                             ı
                                                                                                                                                                                                   Cestrum
                                                                                                                                                                                                                                       plant;
                                                                                                                                                                           Unidentified
                                                                                                                                                                                       Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                     leaf curling virus; Cn
nt; nopaline synthase;
                                                    /*tag= b
/note= "Corresponds
1343..1618
                                                                                           /*tag= a
/note= "CmYLCV CmpS promoter fragment"
411..1331
                                                                                                                                                 Location/Qualifiers
                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 A; 372 C; 390 G;
                                                                                                                                                                                                  yellow leaf curling
                                                                                                                                                                                                                                                                                                                                                      DNA; 1618
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95.8%;
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                                "Nopaline synthase
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                                                                                                                                                                                                                                                                                                                                                      ВP
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome of Cestrum yellow leaf curling e expression of an associated desired
                                                                                                                                                                                                                                     CmYLCV;
                                                                         င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 T; 0 other;
                                                                        SynGFP1
                                   (NOS) terminator"
                                                                                                                                                                                                                                       green
                                                                                                                                                                                                                                       transcription;
green fluorescent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                        protein-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                             vector
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RESULT 13
AAD19840
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
        Chimeric -
Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       times and in most tissues and organs. The present DNA sequence is a promoter-reporter cassette which contains CMYLCV Caps promoter fragment, green fluorescent protein-1 synGFP1 reporter gene and the Agrobacterium tumefaciens nopaline synthase (NOS) terminator. Promoter-reporter cassette is used to construct plant transformation vector.
                                                       ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1618 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                 transgenic
                                                                             Cestrum yellow leaf curling virus; CmYLCV; transcription; maize;
                                                                                                   Ubq3(At)-synGFP1-NOS
                                                                                                                           18-DEC-2001
                                                                                                                                                 AAD19840
                                                                                                                                                                       AAD19840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relates to recombinant DNA sequences containing promoter sequences which are used for creating transgenic plants expressing DNA of interest at all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of associated polynucleotide sequences. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel
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                                                                                                                                                                                                                                                                                                                                                                      CCAAAATTTGTTGATGTGCAGGTACGCGGGTGC
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                                                                                                                                                                                                                                 CCAAAATTTGTTGATGTGCAGGTGCAGGAGCGC
                                                                                                                                                                                                                                                                              ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGA
                                                                                                                                                                                                                                                                                                                           TTAGTAGTAATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                     204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence obtained from genome of Cestrum for conferring constitutive expression of an
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 95.8
04; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNGENTA PARTICIPATIONS
                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stavolone L,
        Arabidopsis thaliana. Agrobacterium tumefaciens. Unidentified.
                                                                 plant;
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2000GB-0010486.
2001EP-0101802.
                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468
                                                                 nopaline
                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%;
95.8%;
                                                                                                    terminator expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 C; 400 G; 367 T; 0 other;
                                                                 synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 198.6; DB 2
Pred. No. 1.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
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                                                                  NOS;
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                                                                 green
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                                                                 fluorescent protein;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are used for creating transgenic plants expressing DNA of interest at all times and in most tissues and organs. The pressing DNA of interest at all Ubq3(At)-synGFP1-NOS terminator expression cassette which comprises Arabidopsis thallana ubiquitin 3 promoter, Ubq3(At) operatively linked with green fluorescent protein-1, synGFP1 reporter gene and Agrobacterium tumefaciens nopaline synthase (NOS) terminator. This expression cassette is used for the construction of plant transformation vectors.
       2191
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28-APR-2000;
26-JAN-2001;
                                                                                                    2131
                                                                                                                                                                                                2071
                                                                                                                                                                                                                                                                                             2011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2943 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 19; Page 93-94; 100pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel DNA sequence obtained from genome of Cestrum yellow leaf virus for conferring constitutive expression of an associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hohn
                                                    201
                                                                                                                                              141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2001;
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                                                                                                                                                                                                                                                                                                            CCAAAATTTGTTGATGTGCAGGTGCAGGAGCGC
                                             CCAAAATTTGTTGATGTGCAGGTACGCGGGTGC
                                                                                       ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGA
                                                                                                                   ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTTATAACTTTTCTAATATATGA
                                                                                                                                                                                    TTAGTAGTAATATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCA
                                                                                                                                                                                                                                                                                TTAGTAGTAATATATTTCAAATATTTTTTCAAAATAAAAGAATGTAGTATAGCA 140
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                                                                                                                                                                                                                                                                                                                                                                                         204;
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2000GB-0007427.
; 2000GB-0010486.
; 2001EP-0101802.
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/note= "Arabidopsis ubiquitin 3
1738..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2670..2943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note "Nopaline synthase (NOS) terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                      9.8%;
95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 544 C;
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                                                                                                                                                                                                                                                                                                                                                                                  Score 198.6;
Pred. No. 1.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 G; 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΑG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ligon HT,
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2223
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                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter,
                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               2943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        curling
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                          2190
                                                                                                                                                                                    2130
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RESULT 14 AAD19830

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GTTGATGTGCAGGTA

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel DNA sequence obtained from genome of Cestrum yellow leaf curling virus for conferring constitutive expression of an associated desired
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 67-68; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide
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28-APR-2000;
          210
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-2001;
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                                                                                                                                                                                                                                                                       90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant
                                                                                                                                                                                                                                                                                                                                                                 GTTGATGTGCAGGTA 224
                                                                                                    CTGTAGTTTATAAGTGTGTGTATATTTTAAATTTATAACTTTTCTAATATATGACCAAAATTT
                                                                                                                                                                                                 ATATAATATTTCAAATATTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT
                                                                                                                                                                                                                                 ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT 149
                                                                 CTGTAGTTTATAAGTGTGTATATTTAATTTATAACTTTTCTAATATATGACCAAAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformation vectors
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2000GB-0010486.
2001EP-0101802.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
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CC comprising the promoter or fragments and a transgenic plant comprising CC the vector. The promoter or fragments are useful for expressing a conclude tide sequence of interest. The transit peptide is useful for cc targeting an associated protein of interest to plastids. A nucleic acid CC which expresses polypeptide having lipoxygenase activity is useful for CC inhibiting fungal mycotoxins when transformed into a plant. The cc inhibiting fungal mycotoxins The promoter is useful for regulating transcription of a chemically inducible but not CC useful for regulating transcription of a chemically inducible but not CC wound or pathogen inducible gene, which involves applying a chemical CC regulator to a plant or seed containing a chemically regulatable CC nucleotide sequence. Transgenic plants as described above are useful for Dreeding improved plant lines that for example increase the effectiveness CC conventional methods such as herbicide or pesticide treatment or allow to dispense with the methods due to their modified genetic properties. CC New crops with improved stress tolerance can be obtained that, due to their optimised genetic equipment yield harvested product of better quality than products that were not able to tolerate comparable adverse CC constitute of the conditions. The present sequence is the glutathione-S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (a promoter of chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving chemically-inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Chimeric -
                                                     transferase (GUS) sequence (containing an intron from solution referred to as GIG) whose expression is driven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Page 75; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of an associated nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-188550/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYGN ) SYNGENTA PARTICIPATIONS AG (UYZU-) UNIV ZUERICH.
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15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     llpoxygenase; RCI-1; transgenic; plant antifungal; pNOV2347;
e chemically induced cDNA; promoter; transit peptide; plastid;
gal mycotoxin inhibitor; plant breeding; glutathione-S-transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIG
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Solanum tuberosum.
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2000GB-0022739
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Sequence 2001 BP;
532 A;
451 C;
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<u>د.</u>
483
T; 0 other;
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οy B В δÃ 밁 Ş 밁 Ş Matches 195; Query Match Best Local Similarity 563 210 503 150 443 383 90 GTTGATGTGCAGGTA GTTGATGTGCAGGTA 224 CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT ATATAATATTTCAAATATTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTT ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT Conservative 577 100.0%; 9.68; 0; Score 195; DB 24 Pred. No. 9e-34; Mismatches DB 24; 0 Length 2001; Indels 0; Gaps 149 442 89 209 562 502

Search completed: May 11, 2003, 18:05:03 Job time: 536.5 secs



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Post-processing: Minimum Match 0%
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Match
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Copyright (c) 1993 - 2003 Compugen
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                                                                                   Description
            BM109636
BQ512568
BQ512569
AL301578
AL071865
AL108567
                       EST557172
EST619983
EST619984
Tetraodon
 Drosophil
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JOURNAL
COMMENT
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BM109636/c
LOCUS
DEFINITION
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AUTHORS
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1 (bases 1 to 675)
van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S., Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
                                                          Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                 mRNA sequence.
BM109636
                                                                                                                                                                                                                                                                                                     BM109636 675 bp EST557172 potato roots Solanum
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                                               primer: T3.
                        Location/Qualifiers
1. .675
/organism="Solanum tuberosum"
/cultivar="Kennebec"
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CNS0170T
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AL069706 Drosophil
AL168150 Tetraodon
B28108 T2G12TRD TA
AL060100 Drosophil
AL062360 Drosophil
B96681 T3001TR TAM
AQ286687 RPCII1-81
AL053529 Drosophil
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BQ596436 PfESTOAD3
AL087992 Arabidops
BQ838839 WHE3593_C
BH438258 BGGLZ67TF
BH178455 011_J 02-
AL615412 T3 end of
AL106896 Drosophil
AQ583787 RPCI-11-4
AL075293 Drosophil
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BH179465 014_p_10-
AQ961004 LERFITS9TF
AL095522 Arabidops
AL053013 Drosophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167;
                                                                                                                                                                                 Email: potato@tigr.org
This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                        The Institute for Genomic Research 9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                Unpublished (2002)
Other_ESTs: EST619984
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                     cdna@resgen.com
Seq primer: T3.
                                                                                                                                                                                                                                                                              Contact: Robin Buell
                                                                                                                                                                                                                                                                                                                                    Generation of a set of
                                                                                                                                                                                                                                                                                                                                                                    Buell, C.R., Hart, A., Baker, B., Restrepo, S., Griffiths, H., van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ512568
BQ512568.1
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/clone_lib-"Generation of a set of potato cDNA clones microarray analyses mixed potato tissues" \,
                                /db_xref="taxon:4113"
/clone="STMHZ22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; supplier: Cornell University, Tanksley lab; sequencing; The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Roots were isolated two weeks after placing the stem cuttings from in vitro grown plants on medium."

a 117 c 100 g 206 t
                                                                                            ∕organism="Solanum tuberosum"
                                                                                                                                  Location/Qualifiers
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/clone_lib="
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/lab_host="SOLR"
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/clone="cPRO4H6"
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Pred. No. 4.9e-18;
0; Mismatches 27;
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a set of potato cDNA clones for microarray
ssues Solanum tuberosum cDNA clone STMHZ22
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Seq primer: T7.
                                                                                                                                                                                                                                                                          This clone is available through the Research Genetics for further inform
                                                                                                                                                                                                                                                                                                                          Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2002)
Other_ESTs: EST619983
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Generation of a set of potato cDNA clones for microarray analyses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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Buell, C.R., Hart, A.,
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                                                                        /clone_lib="Generation of a set of potato microarray analyses mixed potato tissues" /tissue_type="mixed tissues"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Combination of untreated and Phytophthor
infestans-treated libraries of stolons, leaves, leaflets
                                                                                                                                  /db_xref="taxon:4113"
/clone="cmurron:
                                                           /lab_host="SOLR"
                                                                                                                                /clone="STMHZ22"
                                                                                                                                                                                  /organism="Solanum tuberosum"
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XhoI: supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
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/lab_host="SOLR"
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                                                                                                                                                                                                                                                                          rch Genetics, contact the 1-800-711-6195 or
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for microarray
clone STMHZ22
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Submitted (12-APR-2000)
This sequence is a single read
                                                                                                                                                                                         This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
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lt,A., Quetler,F., Saurin,W., Bernot
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Petermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRt digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw Sp, the same strain used for the BDGP's and the force that all the approach of the library or the part of the same strain used for the BDGP's and the force that all the college of the library or the same strain used for the library and but to Order individual BAC Clones the entire library or the same strain used for the library and but to Order individual BAC Clones the entire library or the same strain used for the library or the library or the same strain used for the library and but to Order individual BAC Clones the entire library or the library or the library or the library or library or the library or library o
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                                                                                                                                                                          and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence.
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Chris Town
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
114 c 142 g 200 t
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/strain="TO1000DH3"
/db_xref="taxon:3712"
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Determination of this BAC-end sequence was carried out as par collaboration with the European Drosophila Genome Project (ED/http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                  GSS.
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Drosophila melanogaster.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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BACN37L08 of DrosBAC library from
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Determination of this BAC-end sequence was carried out as collaboration with the European Drosophila Genome Project http://www.edgp.ebi.ac.uk - This Drosophila melanogaster
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   d'Etude
                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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/db_xref="taxon:7227"
/clone="BACN17H15"
/clone_11b="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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Arabidopsis AL089326.1

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survey sequence.
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/plasmid="pBeloBAC11"
/note="end : SP6"
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/db_xref="taxon:7227"
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                                                                 d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                            Drosophila melanogaster.
Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNO3017 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                             Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                     Direct Submission
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Eukaryota; Viridiplantae;
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Rosidae; eurosids II; Brassicales;
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/Strain="Columbia"
/db_xref="taxon:3702"
/clone="T3K15"
/clone=1ib="TAMU"
/note="end : Sp6"
/note="end : Sp6"
a 143 c 141 g 202 t 12
        ∕organism≃"Drosophila melanogaster"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
 Similarity 44.3
74; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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/clone="BACN03017"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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/db_xref="taxon:7227"
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/plasmid="pBeloBAC11"
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   Score 55.8; DB
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SOURCE

657

Insecta; Pterygota;

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JOURNAL
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                                  TTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTTCTGTAGTTTATAAGTGTG
                                                                                                           TAWWWWTATATTATAAAAWAANAWTAWTWAWTANTATTATAWTATATAWWTTWANAAAT 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C. Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 153PO4 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS020N7
                                                                                                                                                                                                                                                                                                                                                                                                                                          genome. For more information, please t
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weissenbach, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene number estimate provided by genome Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bouneau, L., Billault, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                            /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/db_xref="153P04"
/clone="153P04"
/clone_lib="G"
/note="Genoscope sequence ID : COAG153DH02SP1-end
                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                   18;
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                                                                                                                                                                                                   Score 55.6; DB Pred. No. 0.051;
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                                                                                                                                                                WTATWAWATAWATTATTTTTATTATTT 860
                                                                                                                                                                                                                                                        TTTTATTTTTTTTTWWTATTATAATWATWATATAAAAAATATTWTWTWTWAATWRWTTTWT 947
                                                                                                                                                                                                                                                                                                                                   TTTTAATTTATAACTTTTCTAATATAT 198
                                                                                                                                                                                                                                     sequence.
BH179465
BH179465.1
                                                 BH179465
014_P_10-21
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/note="end : TET3"
120 c 103 g
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/db_xref-"taxon:7227"
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GI:16280351
                                                     SmBAC1 Schistosoma
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                                                                                                                                                                                                                                                                                                                                                                                       21;
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Pred. No. 0.05
21; Mismatches
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linear G

GSS 29-OCT-2001 e 014P10 5', DNA

Indels Length

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Gaps

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887

others

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BASE COUNT
ORIGIN
Search completed: May 11, 2003, 23:14:50 Job time: 3319.5 secs
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                                                                                     AATATAATATTTCAAATATTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTT 148
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Schistosoma mansoni.
Schistosoma mansoni
Schistosoma mansoni
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 975)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLATE: 014 POW: P COLUMN: 10
Seq primer: M13 -21 primer
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID=DG0AA014DH05CP1 Bases 255-407 have 95% identity to S.mansoni EST AA269074.1 from base 1-153. Bases 30-538 have 92% identity to S.mansoni EST BF936764.1 from base 512-6.
Plate: 014 row: P column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: 014_P_10-rev
Contact: Pierce RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institut Pasteur de Lille
I rue du Professeur A. Calmette, 59019-Lille, France
                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lbb_host-"Blomphalaria glabrata"
//lbb_host-"Blomphalaria glabrata"
//note-"Vector: pBeloBAC 11; Site_1: Hind III; Partially
Hind III digested and size-selected S. manson1 cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent:
sizing-ligation-transformations. Average insert size
ranges from 70-127 kb and genome coverage is 7.9-fold."
a 116 c 68 g 423 t 87 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Schistosoma mansoni"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="014P10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'dev_stage="cercariae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="SmBAC1"
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Maximum DB
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                                                        GCTCCGGCAGCAAGGGGCGGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA
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                                          GCTCCGGCAGCAAGGGGGCGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA
                                                                                              AGGCGCGTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCTGAC
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                                                          Query Match
Best Local
                                                Matches
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                                                                                                                                                                                                                   TELEFAX: (317) 231-743
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & T
STREET: 11 South Meri
CITY: Indianapolis
STATE: IN
                                                                                                        HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pUMIGIT(
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ramsay, Nichola TITLE OF INVENTION: Contro NUMBER OF SEQUENCES: 3
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TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
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                                                                                                                                                        MOLECULE TYPE:
693
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                        30
                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                           NAME: Breen, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 46204
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                                                                                                                                                                                                       LENGTH:
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                                                          Similarity
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Pred. No.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        TELEFAX: (317) 231-7433 NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                   AOLECCE: NO
                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/123,644
FILING DATE: 28-JUL-1009
                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
150 CTGTAGTTTATAAGTGTGTATATTTTAATTTTATAACTTTTCTAATATATGACCAAAATTT
                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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ITLE OF INVENTION: Method of Using
UMBER OF SEQUENCES: 9
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                                                  ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT 149
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11 South Meridian
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                                                                                                                                          Score 195; DB 3; Pred. No. 3.6e-38; 0; Mismatches 0;
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Best Local (
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GENERAL INFORMATION:
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HYPOTHETICAL: I
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                              150 CTGTAGTTTATAAGTGTGTATATATTTTAAATTTATAACCTTTTCTAATATATGACCAAAATTT
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                                                                                                                90 ATATAATATTTCAAATATTTTTTCAAAATAAAGAATGTAGTATATAGCAATTGCTTTT 149
                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 GTTGATGTGCAGGTA 224
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                                                                                                                                                                                                                                                                             CLONE:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Breen, John P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 26-MA
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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GTTGATGTGCAGGTA 882
                       GTTGATGTGCAGGTA 224
                                               CTGTAGTTTATAAGTGTGTATATTTAATTTATAACTTTTCTAATATATGACCAAAATTT
                                                                                                  ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT
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INVENTION: Contro
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(317) 23
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                                                                                                                                                                                                                                                                                                                                                                                 5534 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Barnes & Thornburg
11 South Meridian
                                                                                                                                                                                                           9.6%;
ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett, Malcolm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                       Score 195; DB 1, Pred. No. 5.1e-38;
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Kriz, Alan L

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В
               RESULT 7
US-09-080-625-1
; Sequence 1, Application US/09080625
; Patent No. 6307123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; I Matches 195; Conservative 0;
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   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTOKNAL.

NAME: Breen, John F.

REGISTRATION NUMBER: 38,833
REGISTRATION NUMBER: 6653
REFERENCE/DOCKET NUMBER: 6653
TELECOMMUNICATION INFORMATION:
TOTAL TO
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ramsay, Nicola
TITLE OF INVENTION: Method of Using Transactivation Proteins to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                    210 GTTGATGTGCAGGTA 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 28-JU
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT 867
                                                                                                                                                                                                      GTTGATGTGCAGGTA 882
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11 South Meridian
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SEQ ID NO 1
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US-09-080-625-1
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09695782
Patent No. 6433252
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                APPLICANT: KRIZ, APPLICANT: GRIFE
NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn Ver.
                                                                        PRIOR FILING DATE: 1998-05-18
                                                                                                                    PRIOR APPLICATION NUMBER: 09/080,625
                                                                                                                                                                                                                                    FILE REFERENCE: DEKM: 161USC1
                                                                                                                                                                                                                                                                    APPLICANT: GRIFFOR, MATTHEW TITLE OF INVENTION: METHODS /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Hanson, Robert F
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REGISTRATION NUMBER: D-42,6
REFERENCE/DOCKET NUMBER: DE
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Arnold White & Durkee
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ZIP: 77210-4433
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(512) 474-7577
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97.5%;
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Pred. No. 5.2e-38;
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US-09-080-625-2
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; OTHER INFORMATION:
US-09-695-782-1
                             Query Match
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Best Local Similarity 97.5%;
Matches 197; Conservative
                                                                                                        TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                         REFERENCE/DOCKET NUMBER: DEI
                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE TITLE OF INVENTION: IDENTIFICATION
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TYPE: DNA
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                                                                            STRANDEDNESS:
                                                                                         TYPE:
                                                                TOPOLOGY:
                                                                                                   LENGTH:
                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                   NAME: Hanson, Robert
REGISTRATION NUMBER:
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                 Similarity
                                                                                    : 3336 base pairs
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     Conservative
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                                                                                                                                                 (512) 418-3000
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               9.6%;
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            Score 194;
Pred. No. 7.
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Pred. No. 5.2e-38;
0; Mismatches 5;
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  Mismatches
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  DB 4; I
'.1e-38;
les 5;
                       Length 3336;
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; OTHER INFORMATION: Primer
US-09-695-782-2
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            Sequence 4, Application US/09080625
Patent No. 6307123
GENERAL INFORMATION:
APPLICANT: Kriz, Alan L.
APPLICANT: Spencer, T. Michael
APPLICANT: APPLICANTION: METHODS AND
TITLE OF INVENTION: IDENTIFICAT:
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PRIOR FILING DATE: 1998-05-18
NUMBER OF SEO ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 2
LENGTH: 3336
TYPE: DNA
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Best Local :
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE IDENTIFICATION
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 NUMBER OF
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SEQUENCES:
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            METHODS AND COMPOSITIONS FOR TRANSGENE IDENTIFICATION
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Pred. No. 7.1e-38;
0; Mismatches 5
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                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                           Sequence 4, Applia Patent No. 643325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 97.5 Matches 197; Conservative
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ZIP: 77210-4435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPARE PC-DOS/MS-DOS
                                                                                                                                                              APPLICANT: GRIFFOR, MATTHEW
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE IDENTIFICATION
FILE REFERENCE: DEKM:161USC1
CURRENT APPLICATION NUMBER: US/09/695,782
CURRENT FILING DATE: 2000-10-24
                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                              PRIOR APPLICATION NUMBER: 09/080,625 PRIOR FILING DATE: 1998-05-18
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SEQUENCE CHARACTERISTICS:
LENGTH: 3877 base pairs
                                                                                                                                                                                                                              APPLICANT: KRIZ, ALAN L.
APPLICANT: GRIFFOR, MAT
                    ORGANISM: Artificial Sequence
FEATURE:
                                                  TYPE: DNA
THER INFORMATION: Description of Artificial Sequence:
                                                              ENGTH: 3877
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NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-4
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CURRENT APPLICATION DATA:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                              AAAATTTGTTGATGTGCAGGTA 2183
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(512) 474-7577
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Pred. No. 7.6e-38;
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LENGTH: 5560
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Patent No. 6074876
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Best Local
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CURRENT FILING DATE: 1997-05-15
EARLIER APPLICATION NUMBER: PCT/EP96/03366
EARLIER FILING DATE: 1996-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1995-08-04 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GENETIC TRANSFORMATION USING FILE REFERENCE: 2121-0127P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: EP 95401844.6
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                                                                                          LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU:
OTHER INFORMATION: gene (
                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (318)..(869)
OTHER INFORMATION: bar: region coding for phosphinotricin
                                                                                                                                                                                                                                                                                                            LOCATION: (84)..(296)
OTHER INFORMATION: 3' 97:
                                     NAME/KEY: misc_feature
LOCATION: (2765)..(305
                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                      OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                                                                                            OTHER INFORMATION: polyadenylation OTHER INFORMATION: T-DNA
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
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                                   . (3058)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description plasmid pTHV
3' untranslated region of the CaMV containing polyadenylation signals
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of Arabidopsis t)
                                                                                                                                                                                                                                                                                           3' untranslated region containing the
enylation signal of gene 7 of Agrobacterium
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                    transcript
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: OTHER INFORMATION: region with unknown sequence (may contain ) OTHER INFORMATION: nucleotides)
US-08-817-188-5
                                                                                                                                                                    Sequence 2, Application US/09367293
Patent No. 6444878
GENERAL INFORMATION:
APPLICANT: Donaldson, Lain A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                     FILE REFERENCE: DYOU21.001APC
CURRENT APPLICATION NUMBER: US/09/367,293
CURRENT FILING DATE: 1999-12-23
                                                                                  APPLICANT: Jorgensen, Kirsten
APPLICANT: Jorsboe, Morten
TITLE OF INVENTION: SELECTION METHOD FOR
FILE REFERENCE: DYOUZ1.001APC
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                           PRIOR APPLICATION NUMBER: PCT PRIOR FILING DATE: 1998-02-05
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LOCATION: (5077)...(5078)
OTHER INFORMATION: region with unknown
OTHER INFORMATION: nucleotides)
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OTHER INFORMATION: region with unknown sequence
OTHER INFORMATION: nucleotides)
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LOCATION: (5476)..(547
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LOCATION: (5533)..(5560)
OTHER INFORMATION: LB: left
OTHER INFORMATION: pTIB6S3
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LOCATION: (4483)..(4671)
OTHER INFORMATION: IV2: region corresponding
OTHER INFORMATION: the ST-LS1 gene
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LOCATION: (3059)..(5056)
OTHER INFORMATION: uida:
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APPLICATION NUMBER: GB FILING DATE: 1997-02-07
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Pred. No. 7.6e-37;
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; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein B
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                                                                                                                                                                                    Query Match
Best Local S
Matches 238
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Best Local Similarity
Matches 190; Conserv
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SOFTWARE: FastSEQ for
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/249,585A CURRENT FILING DATE: 1999-02-11
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                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Horlick,
                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)..(1926)
OTHER INFORMATION: template strand of EBNA-1 DNA
                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 0867/0D905
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                 1675
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10 US-09-887-576-581

10 US-09-969-37-1213

10 US-09-969-37-1213

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Sequence 1, Appli	Sequence 36, Appl	Sequence 209, App	Seguence 1, Appli	Sequence 1212, Ap	Sequence 368, App	e 739,	•	Sequence 96, Appl	Sequence 67, Appl	Sequence 1, Appli	188, 7	Sequence 119, App	Sequence 109, App	1,	Sequence 1, Appli	 Sequence 6529, Ap 	Sequence 64, Appl	Sequence 94, Appl	•	Sequence 18, Appl	Sequence 857, App	Sequence 20, Appl	e 11	Sequence 9, Appli	Sequence 212, App

ALIGNMENTS

US-09-940-550A-9

Sequence 9, Application US/09940550A Publication No. US20030033635A1 GENERAL INFORMATION:

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; SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 9
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Best Local Similarity
Matches 2031; Conserv
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PRIOR APPLICATION NUMBER: 60/227,961
PRIOR FILING DATE: 2000-08-25
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APPLICANT: MCKERSIE, BYVAN
TITLE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 16313-0055
                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                             TACCGCATTCAGCGCGACCCGATCACGCTCCGGCCGGTCGAGCTTGATTGCGGACCGATC
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US-09-940-550A-10

Sequence 10, Application US/09940550A

Publication No. US20030033635A1

GENERAL INFORMATION:

APPLICANT: MANKIN, LUKE

APPLICANT: MCKERSIE, BRYAN

TITLE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF

FILLE REFERENCE: 16313-0055

CURRENT APPLICATION NUMBER: US/09/940,550A

CURRENT FILING DATE: 2001-08-27

PRIOR APPLICATION NUMBER: 60/227,961

PRIOR FILING DATE: 2000-08-25

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 10

LENGTH: 2031

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: C31int* DNA

US-09-940-550A-10

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	CCGCTTCA 1020	961 CGCATGGACGCTGACGCCGTGCCGACCCGGGGCGAGACGATTGGGAAGAAGACACAC	
	CGCTTC	GCATGGACGCTGACGCCGTGCCGACCCGGGGCGAGACGATTGGGAAA	
	CTTTGTAAG 960 CTTTGTAAG 960	901 CCCTTCAAGCCGGGCAGTCAAGCCGCCATTCACCCGGGCAGCATCACGGGGC	
	ACACCIT 9	41 GAGTTCGAGCCCGACGTAATCCGGTGGTGGTGGCGTGAGATCAAGACGCA	
	ACCCTTC 84	GTCAATGTCGTCATCAACAAGTTAGCGCACTCGACCACTCCCCC	
	GACCCTTC 840	81 ATGGTCAATGTCGTCATCAACAAG	
	NACGGCCGA 780	721 AAGGCGCCTTACGGCTTCGAGCTTGTTTCGGAGACGAAGGAGGAGATCACGCGCAA	
	FICGECEGE 720	661 TCGGCGAAGATTCTCGACACGAAGAACCTTCAGCGCGAATTGGGCGGGTACG	
	CGCTGAAG 66	01 AT	о О
	CGCTGAAG 66	01 ATGGACCTGATTCACCTGATTATGCGGCTCGACGCGTCGCACAAAGAAT	y 6
,	GAAACGTC 600	541 CTCGCCCTGGGCGTGACGATTGTTTCCACTCAGGAAGGCGTCTTCCGGCAGG	
	CGGAATTG 540	481 GACGTGTCGCGCTTCTCGCGCCTGAAGGTCATGGACGCGATTCCGATTGTCT	
	 TTGTCTAT 480	421 GAGTTCGAACGCATCCTGAACGAATGCCGCCCGGCCGGCGCCCAACATGATCA	
	TTGTCTAT 48	21 GAGTTCGAACGCATCCTGAACGAATGCCGCGCGCGGGCGG	4
)AGCGCCCG 420 AGCGCCCG 420	361 TTCGTCGGGCATTTCAGCGAAGCGCCGGGCACGTCGGCGTTCGGGACGGCGG	
	GGTTCAGG 360 GGTTCAGG 360	301 AACGAAGACAAGGCGGCCGACCTTCAGCGCGAAGTCGAGCGCGACCGAGCGGGGCC 	
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	GCC 30	41 CGTCAGTCGCGCGAGCGCGAGAATTCGAGCGCAGCAAGCCCAGCGACACAC	N
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0;	0; Gaps	y Match 99.2%; Score 2015; DB 9; Length 2 Local Similarity 99.5%; Pred. No. 0; hes 2021; Conservative 0; Mismatches 10; Indels	Query Best Match

•	1981 GACGACGAAGAAGACGACGCCAAGGACGGCACGGAAGACGTAGCGGCGTAG 2031 	Qу
1980 1980	1921 AGGGGCAGGGAACGCCCATCGAGAAGCGCGCTTCGATCACGTGGGCGAAGCCGCCGACC	Qy Db
1920 1920	1861 AAGCGCGTGTTCGTCGGCTCTTCGTAGACAAGATCGTTGTCACGAAGTCGACTACGGGC	Qy Db
1860 1860	1801 GACGCCGACGCTGACCCGACCGGCCCTAAGTCGTGGTGGGGGGCGCGCGTCAGTAGACGAC	Qy Db
1800	1741 CTTGCCGAACTTGAAGCCGCCGAAGCCCCGAAGCTTCCCCTTGACCAATGGTTCCCCGAA :	Qy Db
1740 1740	1681 AAGCACTTCCGGAAGCAACAGGCAGCGCTGACGCTCCGGCAGCAAGGGGCCGGAAGAGCGG :	Qy Db
1680 1680	1621 GCCCTTGAAGAGCTGTACGAAGACCGCGCGGCGGAGGCGCGTACGACCCGTTGGCAGG	Qy Db
1620 1620	1561 GCGCCTGAGAAGAGCGGCGAACGGGCGAACCTTGTTGCGGAGGCGCCGCGACGCCCTGAAC :	Qy Db
1560 1560	1501 GACGAAGAGACGTTGGCGCTTCTGTGGGAAGCCGCCGGCGACGCTTCGGCAAGCTCACTGAG :	Db Qy
1500 1500	1441 GCGGCACTCGACAAGTTCGTTGCGGAACGCATCTTCAACAAGÁTCAGGCACGCCGAAGGC :	Qу Db
1440 1440	1381 CGGAAGGTGGTCGACCCGTCCGCACCTGGGCAGCACGAAGGCACGTGCAACGTCAGCATG :	Qу
1380 1380	1321 GCCGTCATGACTTCGAAGCGCGGGGAAGAATCGATCAAGGACTCTTACCGCTGCCGTCGC :	Db Db
1320 1320	1261 GGGCTTTCCCGGGGGCAAGCCATTCTGTCCGCCATGGACAAGCTGTACTGCGAGTGTGGC :	Qу
1260 1260	1201 ATCGAGCCCGCTGAGTGGTATGAGCCTTCAGGCGTGGTTGGACGGCAGGGGGCCCGGCAAG :	Фр
1200 1200	1141 TACCGCATTCAGCGCGCACCCGATCACGCTCCGGCCGGTCGAGCTTGATTGCGGACCGATC :	Оу
1140 1140	1081 GCCGCTGAGGTGATCTACAAGAAGAAGCCGGACGGCACGCCGACCACGAAGATTGAGGGT :	Оу
1080 1080	1021 AGCGCCTGGGACCCGGCAACCGTTATGCGAATCCTTCGGGACCCGCGTATTGCGGGCTTC 1 	Qy Db

RESULT 3
US-09-940-550A-11
; Sequence 11, Application US/09940550A
; Publication No. US20030033635A1

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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: a, t, C NAME/KEY: modified_base LOCATION: (5233)
OTHER INFORMATION: a, t, C NAME/KEY: modified_base LOCATION: (8478)
OTHER INFORMATION: a, t, C NAME/KEY: modified_base LOCATION: (8480)
OTHER INFORMATION: A, t, C NAME/KEY: modified_base LOCATION: (8480)
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NAME/KEY: modified_base
LOCATION: (1986)
OTHER INFORMATION: a, t, c
NAME/KEY: modified_base
LOCATION: (5231)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/940,550A CURRENT FILING DATE: 2001-08-27 PRIOR APPLICATION NUMBER: 60/227,961 PRIOR FILING DATE: 2000-08-25 PRIOR SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JENERAL INFORMATION:
APPLICANT: MANKIN, LUKE
APPLICANT: MCKERSIE, BRYAN
TITLE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 16313-0055
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ORGANISM: Artificial Sequence
FEATURE:
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                GCGCCCGGAGTTCGAACGCATCCTGAACGAATGCCGCCGGCGGCGGCTCAACATGATCAT 473
GTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCGGGCACGTCGGCGTTCGGGACGGCGGA 413
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Db Db	474 5464	TGTCTATGACGTGTCGCGCTTCTCGCGCCCTGAAGGTCATGGACGCGATTCCCGATTGTCTC 533	
Qy	G.	GGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCAGGAAGGCGTCTTCCGGCAGGG 59	
Db	5524	Ü	
Qy	594	CATGGACCTGATTCACCTGATTATGCGGCTCGACGCGTCGCACAAAGAATCTT	
DЬ	5584	CGTCATGGACCTGATTCACCTGATTATGCGGCTCGACGCGTCGCACAAAGAATCTTC 5	
Qy	654	GGCGAAGATTCTCGACACGAAGAACCTTCAGCGCGAATTGGGCGGGTACG	
Db	5644	HAGTCGGCGAAGATTCTCGACACGAAGAACCTTCAGCGCGAATTGGGCGGGTACGT	
Qy	. 714	ACGGCTTCGAGCTTGTTTCGGAGAGCGAAGGAGTCACGC	
Дb		GGCGGGAAGGC	
Qy	774	ACTCGACCACTCCCCTTAC	
Db	5764	GGCGAATGGTCATCATCAACAAGCTTGCGCACTCGACCACTCCCCTTACCG	
Qy	834	CCTTCGAGTTCGAGCCCGACGTAATCCGGTGGTGGTGGCGTGAGATCAAGACGCAC	
Db	5824	CCTTCGAGTTCGAGCCCGACGTAATCCGGTGGTGGTGGTGAGATCAA	
Qy	8	ACACCTTCCCTTCAAGCCGGGCAGTCAAGCCGCCATTCACCCGGGCAGCATCACGGGGCT 953	
Дb		CACCTTCCCTTCAAGCCGGGCAGTCAAGCCGCCATTCACCCGGGCAGCATCACGGGGC	
Qy	954	TTGTAAGCGCATGGACGCTGACGCCGTGCCGACCCCGGGGGGGAGAGATTGGGAAGAAGAC 1013	
Db	4	SGACGCTGACGCCGTGCCGACCCGGGGCGAGACGATTGGGAAGAAGA	
Qy	1014	GCGCCTGGGACCCGGCAACCGTTATGCGAATCCTTCGGGACCCGCGTATTG	
Дb	6004	GCTTCAAGCGCCTGGGACCCGGCAACCGT	
Qy	1074	CAAGAAGAAGCCGGGACGGCACGCCGACCAAG	
Db		TCGCCGCTGAGGTGATCTA	
Qy	1134	CATTCAGCGCGACCCGATCACGCTCCGGCCGGTCGAGCTTGATTGCG	
Db	6124	AGGGTTACCGCATTC	
Qy	1194	SAGCTTCAGGCGTGGTTGGACGGCAGGGGC	
DЪ	6184	CGATCATCGA	
Qy	254	CTGTCCGCCATGGACAAGCTGTACTGCG	
· Db	44	CAAGGGGCTTTCCCGGG	
Qy	1314	GGGAAGAATCGATCAAGGACTCTTACCC	
Db	6304	TGTGGCGCCGTCATGACTTCGAAG	
Qy	1374	ACCTGGGCAGCACGAAGGCACGTGCAACG	
Db	6364	CGTCGCCGGAAGGTGGTCGACCC	
Qy	1434	NAGTTCGTTGCGGAACGCATCTTCAACAAGATCAGGCACG	
DЬ	424	AGCATGGCGGC	
Qy	1494	GTTGGCGCTTCTGTGGGAAGCCGCCCGACGCTTCGGCAAGC	
DЬ	484	GAAGGCGACGAAGAGAC	

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GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                        APPLICANT: Calos, Michele P.
APPLICANT: SCIIMENTI, Christopher R.
TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME
FILE REFERENCE: 8400-0011
CURRENT APPLICATION NUMBER: US/09/788,297
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
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                                                               AGTCGAGCGCGACGGGGCCGGTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCCGGGCAC
                                                                                                                    AGCAAGCCCAGCGACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA 332
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  CGGGCGCTCAACATGATCATTGTCTATGACGTGTCGCGCCTTCTCGCGCCCTGAAGGTCAT
                                  GTCGGCGTTCGGGACGGCGGAGCGCCCGGAGTTCGAACGCATCCTGAACGAATGCCGCGC
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                       GTCGGCGTTCGGGACGGCGGAGCGCCCGGAGTTCGAACGCATCCTGAACGAATGCCGCGC
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Pred. No. 0;
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PATENT NO. US/0020094516A1
GENERAL INFORMATION:
APPLICANT: Calos, Michele P.
APPLICANT: Sclimenti, Christopher R.
APPLICANT: INVENTION: ALTERED RECOMBINASES FOR
FILE REFERENCE: 8400-0011
                                                                                                                                  Query Match
Best Local Similarity
Matches 1811; Conser
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
SEQ ID NO 26
LENGTH: 1842
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CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 34
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Calos, Michele P.
APPLICANT: Sclimenti, Christopher R.
APPLICANT: Sclimenti, Christopher R.
TITLE OF INVENTION: ALTEERED RECOMBINASES FOR GENOME MODIFICATION
FILE REFERENCE: 8400-0011
CURRENT APPLICATION NUMBER: US/09/788,297
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 1839
TYPE: DAN
ORGANISM: Artificial Sequence
FEATURE:
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US-09-788-297-27
; Sequence 27, Application U:
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Patent No. US20020094516A1
GEMERAL INFORMATION:
APPLICANT: Calos, Michele P.
APPLICANT: Scilmenti, Christopher R.
APPLICANT: Scilmenti, Christopher R.
FILE REFERENCE: 8400-0011
                                                                                                           CURRENT APPLICATION NUMBER: US/09/788,297
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: ALM, T
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promothers for regulation of players.
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
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      PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Budworth, P.

APPLICANT: Brown, D.

APPLICANT: Chang, H.

APPLICANT: Chang, H.

APPLICANT: Zhu, T.

APPLICANT: Wang, X.

APPLICANT: Cooper, Bret

TITLE OF INVENTION: Promoters for regulation of plant expression

FILE REFERENCE: 1360.001US1

CURRENT APPLICATION NUMBER: US/09/887,576

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR APPLICATION NUMBER: US 60/258,692

PRIOR APPLICATION NUMBER: US 60/258,692
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LENGTH: 11180
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
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SEQ ID NO 582
LENGTH: 2000
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Best Local Similarity
Matches 195; Conserv
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                                                                   ATATAATATTTCAAATATTTTTTTCAAAATAAAGAATGTAGTATTATGCAATTGCTTTT 149
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tive 0; Mismatches
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; SEQ ID NO 1213
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1213
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                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/969,373 CURRENT FILING DATE: 2001-10-02
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APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE, REFERENCE: 38-10(52679)A
                                                                                                                                                                                                                   URRENT APPLICATION NUMBER: US/09/791,279
URRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                   ILE REFERENCE:
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ITLE OF INVENTION: NO. L.
00048.US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 ATAAATATGTTCTACTACTAATAAATAATATATAT 92
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                                                                       APPLICATION NUMBER: 00/.
                                                                                                                                             FILING DATE: 2000-02-24
APPLICATION NUMBER: 60/
FILING DATE: 2000-02-24
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FILING DATE: 2000-02-24
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                                    APPLICATION NUMBER
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92; Conservative
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US20020133852A1
                                                                                                                                                                                                                                                                               Lind, Peter
                                                                                                                                                                                                                                                                                                    Parodi, Luis
                                                                                                                                                                                                                                                                                                                                 Vogeli, Gabriel
                                                                                                                                                                                                                                                                                                                   Linda S.
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58.6%;
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                                 60/184,604
                                                                60/184,602
                                                                                                60/184,606
                                                                                                                                 60/184,712
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60/184,822
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Pred. No. 0.005;
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-222
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Best Local Similarity
"atches 82; Conserva
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-279-27
                                                                                                                                                 NUMBER OF SEQ ID NOS: 228
SEQ ID NO 222
LENGTH: 14708
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                    Query Match
Best Local Similarity
                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No.
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11188 GTTTTTGCGTTTGTTTTAGTTGGATTTTTTTTTTTTATTAGTTAAAATGTTATTTTTA 11247
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SOFTWARE: PatentIn version 3.0
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                      722 TATATATAAATAT 734
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FILING DATE: 2000-02-24
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o. US20030082609A1
                                                       Conservative
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האיים OCK, Christian
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                                                                   Score 50; DB 9
Pred. No. 0.29;
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Pred. No. 0.023;
                                                      Mismatches
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                                                                                  DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RAPPOLD-HOERBRAND, GUDRUN
APPLICANT: RAO, ERCOLE
TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT STATURE GENE REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1997-09-29
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                            LOCATION: (2880)
OTHER INFORMATION: a, c,
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LOCATION: (1498)..(1807)
OTHER_INFORMATION: part of exon
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OTHER INFORMATION: a, c,
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LOCATION: (11620)...(11729)
THER INFORMATION: part of
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LOCATION: (4545)..(4619)
DTHER INFORMATION: pET92
                                      OCATION: (3508)
THER INFORMATION: a, c,
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NOCATION: (2665)
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JOCATION: (5305)..(551
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OCATION: (4326)..(4437)
THER INFORMATION: PET92
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OCATION: (3844)..(4068)
THER INFORMATION: pET92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: EP/97100583.0
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               NAME/KEY: misc_feature LOCATION: (4376)
                                                  LOCATION: (4212)
OTHER INFORMATION: a,
                                                                   NAME/KEY: misc_feature LOCATION: (4212)
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OTHER INFORMATION: a,
                                                                                                                      NAME/KEY: misc_feature LOCATION: (4174)
                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (3965)
OTHER INFORMATION: a,
                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: (3729) OTHER INFORMATION: a, c,
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OTHER INFORMATION: a, c,
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OTHER INFORMATION: a,
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OTHER INFORMATION: a,
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OTHER INFORMATION: a,
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LOCATION: (3600)
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US-10-239-676-117; Sequence 117, Application No. US20; Publication No. US20; GENERAL INFORMATION:
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                                                   PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
                                                                                                                          CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                              TITLE OF INVENTION: Diagnosis of Diseases FILE REFERENCE: 5013.1003
                                                                                                                                                                                                              APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
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CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 09/147,699
PRIOR FILING DATE: 1999-06-24
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PRIOR FILING DATE: 1996-10-01
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TITLE	REFERENCE	KEYWORDS SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 1 AX394183 LOCUS
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                                        TAGCGCCAACGAAGACAAGGCCGGCCGACCTTCAGCGCGAAGTCGAGCGCGACGGGGGCCC 353
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GTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCCGGGCACGTCGGCGTTCGGGACGGCGGA 413
                                                                                 CGTC-----AGTCGCGCGAGCGCGAGAATAGCAGTGCAGCAAGCCCAGCGACACAGCG 293
                                                                                                                                                                                                          TAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGAAGTCGAGCGCGACGGGGGCCG
                                                                     CGTCGRCNTNDAGTCGCGCGAGCGCGAGAATTCGAGCGCAGCAAGCCCAGCGACACAGCG
                                                                                                                  ATAACTTTTCTAATATATGACCAAAATTTGTTGATGTGCAGGTACGCGGGTGCTTACGAC 5223
                                                                                                                              ATAACTTTTCTAATATATGACCAAAATTTGTTGATGTAGGAGGTACGCGGGTGCTTACGAC 240
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/db_xref="taxon:32630"
/note="pbes EW051 T-DNA region"
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Bacteriophage phi-C31.
Bacteriophage phi-C31
Viruses; dsDNA viruses, no
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x59938
x59938.1 GI:14903
                                                                                                                                                                                        Kuhstoss,S. and Rao,R.N.
Analysis of the integration function
bacteriophage phi C31
J. Mol. Biol. 222 (4), 897-908 (1991)
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                /rpt_type=INVERTED
                                                                                   /organism="Bacteriophage phi-C31"
/db_xref="taxon:10719"
/map="38158-40368nt (standard phiC31 map)"
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rpt_type=DIRECT
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/transl_table=11
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ILDTKHLQRELGGYVGGKAPYGFELVSETKEITRNGRWNVVILKLAHSTTPLTGFFE
FEPDVIRWWREIKTHKHLPFKPGSQAAIHPGSITGLCKRMDADAVPTRGETIGKKTA
SSAWDDATVMRILRDPRLAGFAAEVIYKKKPDGTPTTKIEGYRJORDPITLRPVELDC
GPIIEPAEWYELQAWLDGRGRGKGLSRGQAILSAMDKLYCECGAVMTSKRGEESIKDS
YRCRRRKVVDPSAPGQHEGTCNVSMAALDKFVAERIFNKIRHAEGDEETLALLWEAAR
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/db_xref="GI:14904"
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Cloning vector pSET152
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Bohm,I., Mironenko,T., Deacon,M., Wheatcroft,M.,
Staunton,J. and Leadlay,P.F.
Increasing the efficiency of heterologous promote
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Submitted (28-SEP-2001) Wilkinson C.J.,
University of Cambridge, 80 Tennis Cour
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Wilkinson, C.J.
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J. Mol. Microbiol.
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                                                                                                                                                                                                                                                                                                                                                                                                    /specific_host="Streptomyces sp."/db_xref="taxon:173260"/lab host="Force"/lab host="Force"/
/note="puc18"
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/translation="MITHSISRAAADPLESTCSPSLALAVVLQRRDWENPGVTQLNRL
                                                                                                                                                                                                                                                                                                                  complement(163. .507)
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                                                                                                                                                           /product="lacz alpha peptide"
/protein_id="CAC93946.1"
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/function="blue-white
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                                                                                                                CGGGCGCTCAACATGATCATTGTCTATGACGTGTCGCGCTTCTCGCGCCCTGAAGGTCAT
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      GGAAGGCGTCTTCCGGCAGGGAAACGTCATGGACCTGATTCACCTGATTATGCGGCTCGA
                                   GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA
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/direction=RIGHT
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KVPYGVPRHCTILQDGKLVPDYLENHCEERFALADRWLKEKSLQKEGPVGHAFARL
KVPYGVPRHCTILQDGKLVPDYLENHCEERFALADRWLKEKSLQKEGPVGHAFARL
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/db_xref="GI:17974212"
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/function="apramycin
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Bacteriophage phi-C31
Viruses; dsDNA viruses, no
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C gene; dCMP deaminage
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WRNVWQAGMGAYSPDTDRNVILRYCELHDRRADLLSLIEADGYMSEGYNGQPVAHPML
RYVESTEKELRSIETAIGFTPEARMRLGIVAAEARKVAAGPEDF"
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/gene="32"
                                                                                                                                                                                              EDDEDDA"
                                                                                                                                                                                                                                                                          IDADGNEVLLGWFTPRDVLHIPGMMLPGDFVGCSPISYARESIGLALAAQKYGŠKFFA
NGAMPGAVVEVPGTMSEEGLARAREAWRAANSGVDNAHRVALLTEGAKFSKVAMSPDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="SPTREMBL:Q9ZXB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'db_xref="GI:3947453"
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/protein_id="CAA07105.1" /db_xref="GI:3947454"

xref="SPTREMBL:Q9ZXB1"

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                                                                           GSELKKKPVRNALPTYEGTLEGEFSAASLGLYDAFV$GEVCSFKATFFGILPGSSLSV
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5144. .6512
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213 GATGTGCAGGTACCGCGGGTGCTTACGACCGTCAGTCGCGGGGAGGGGGGGAGAATAGCAGTGC 272
CCTTCGGGACCCGCGTATTGCGGGCTTCGCCGCTGAGGTGATCTACAAGAAGAAGCCGGA
                                                                                                                                                                                CCCGGGCAGCATCACGGGGCTTTGTAAGCGCATGGACGCCTGACGCCGTGCCGACCCGGGG
                                                                                                                                                                                                                                                                                                                                          CGAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCGAAT
                                                                                                                                                          CCCGGCCAGCATCACGGGCTTTGTAAGCGCATGGACGCCGTGACGCCGTGCCGACCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAGCCCAGCGACACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA 332
                                                                                                                                                                                                                                                    GCGTGAGATCAAGACGCACAAACACCTTCCCTTCAAGCCGGGCAGTCAAGCCGGCCATTCA
                                                                                                                                                                                                                                                                          GCGTGAGATCAAGACGCACAAACACCTTCCCTTCAAGCCGGGCAGTCAAGCCGCCATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                     GACGAAGGAGATCACGCGCAACGGCCGAATGGTCAATGTCGTCATCAACAAGCTTGCGCA 39043
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACGAAGGAGATCACGCGCAACGGCCGAATGGTCAATGTCGTCATCAACAAGTTAGCGCA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGCGAATTGGGCGGGTACGTCGGCGGGAAGGCGCTTACGGCTTCGAGCTTGTTTCGGA 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTCGAGCGCGACGGGGGCCGGTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCGGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCGAATTGGGCGGGTACGTCGGCGGGAAGGCCCCTTACGGCTTCGAGCTTGTTTCGGA 38983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGATTCTCGACACGAAGAACCTTCA 38923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGAATTCTCGACACGAAGAACCTTCA 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAGGCGTCTTCCGGCAGGGAAACGTCATGGACCTGATTCACCTGATTATGCGGCTCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGCGCCTCAACATGATCATTGTCTATGACGTGTCGCGCCTTCTCGCGCCCTGAAGGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGGCGGCTCAACATGATCATTGTCTATGACGTGTCGCGCCTTCTCGCGCCCTGAAGGTCAT 512
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EVU84006 Circular SYN 03-MAY-1997 EXPRESSION vector pBSII-LUCINT firefly luciferase (LUCINT), beta-galactosidase (lac2) and beta-lactamase (ampR) genes, complete cds and lac operon promoter sequence.
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Plant Mol. Biol. Rep. (1997) In press
2 (bases 1 to 5967)
Mankin, S.L., Allen, G.C. and Thompson, W.F.
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1 (bases 1 to 5967)

Mankin,S.L., Allen,G.C. and Th Introduction of a Plant Intron
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NC 27695-7612, USA
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                                                                                                                                                                                                                       /gene="lacz"
3146. .3355
/gene="lacz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFFEAKVVDLDTGKTLGVNQRGELCV
RGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVR
FSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRS
LQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEVGEAVAKRFHLP
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/protein_id="AAB53627.1"
/protein_id="AAB53627.1"
/db_xref="G1:2071945"
/translation="MEDAKNIKKGPAPFYPLEDGTAGEOLHKAMKRYALVPGTIAFTD
/AHIEVNITYAEYFEMSYRLAEAMKRYCLNTNIRIVVCSENSLOFFMPYLGALFIGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="chimera plasmid consisting of a pBS-type plasmid (pLuk07, dsDNA) derived from the LUC* gene (a synthetic cDNA gene) by the addition of a plant intron sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Expression vector
/db_xref="taxon:56405"
/plasmid="pLuk07"
                                                                                                                                                                                                                                                                                                                                                       /gene="LUCINT"
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="LUCINT"
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                               /gene="ampR"
/function="ampicillin
                                                               /gene="ampR"
3895. .4755
                                                                                                              /translation="MAVVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQ
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                                                                                                                                             /protein_id="AAB53629.1"
/db_xref="GI:2071947"
                                                                                                                                                                          /transl_table=11
/product="beta-galactosidase"
                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                         /gene="LUCINT"
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/EC_number="1.13.12.7"
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AX259239
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                                               ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGA
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Cestrum yellow leaf curling virus pr
Patent: WO 0173087-A 37 04-OCT-2001;
Syngenta Participations AG (CH)
Location/Qualifiers
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                                                                                                                                                            Similarity
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/db_xref="taxon:32630"
/note="arrificial sequence synthetic
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/note="lac operon promoter"
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DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDMMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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/protein_id="AAB53628.1"
/db_xref="GI:2071946"
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Pred. No. 2.1e-27;
0; Mismatches 9;
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AX259242
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TITLE
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                                                                      Hohn,T., Stavolone,L., de Haan,P.T.,
Cestrum yellow leaf curling virus pr
Patent: Wo 0173087-A 40 04-OCT-2001;
Syngenta Participations AG (CH)
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Sequence 40 from Patent
AX259242
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Patent: WO 0173087-A 42 04-OCT-2001;
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                 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="artificial sequence Cmps
                                                     1. .1618
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/db_xref="taxon:32630"
/note="artificial sequence CmpC-synGFPI-nos
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AX259240
Sequence
AX259240
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Sequence 48 from Patent W00173087.
AX259250
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                                                                                                                                                                                                                                                                                                                                                                                synthetic
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/db_xref="taxon:32630"
/note="artificial sequence Ubq3(At)-synGFPI-nos expression
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Pred. No. 2.6e-27;
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Pred No. 2.3e-27;
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Cestrum yellow leaf curling virus pr
Patent: WO 0173087-A 38 04-OCT-2001;
Syngenta Participations AG (CH)
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Syngenta Participations AG (CH) ; Universitaet
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451 c 535 g 483 t
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Unclassified.
1 (bases 1 to 2633)
1 (bases 1 to 3633)
Rennett,M., May,S. and Ramsay,N.
Method of using transactivation proteins to control gene expression in transgenic plants
Patent: US 5801027-A 2 01-SEP-1998;
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Sequence 2 from patent US 5801027.
AR037156
AR037156.1 GI:5955012
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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WPI; 2002-280939/32.

New self-excising polynucleotides, useful for producing transgenic

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2 3.	25-AUG-2000; BADI) BASF	AUG-2001;	FEB-2002	WO200216609-	Synthetic.	Phi C31 integrase; recom agricultural food productions; ds; phiC31int*INT.	encoding	JUN-2002	АВК12556;	12556		51.8	51.8	52.2 8.2	53	53 53	53.6	58.2	137.4	137.8	180.6	180.6	181.4	190.8 190	192	194	195 194	195	195 195	195	195	195	198.6	198.6	198.6
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Query Match
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                                                                                   The invention describes an isolated excisable polynucleotide, which comprises a desired trait polynucleotide and a recombinase polynucleotide operably linked to a promoter, all flanked by a pair of directly oriented recombination sites where the recombinase activity is regulatable. The self-excising polynucleotide is useful for producing transgenic plants, particularly for removing all transgenic nucleic acid sequences that encode a gene product from the transgenic plant, thus restoring the original genetic configuration of the genome. The polynucleotide is also useful in methods for eliminating unwanted nucleic acids in agricultural food products and for preventing the escape of certain transgenic traits into the environment. This sequence encodes the novel phic31 integrase phic31intINT, created for use in the self-excising polynucleotide
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                                                      CGCATGGACGCTGACGCCGTGCCGACCCCGGGGCGAGACGATTGGGAAGAAGACCGCTTCA
                                                                                                                                                                      GAGTTCGAGCCCGACGTAATCCGGTGGTGGTGGCGTGAGATCAAGACGCACAAACACCTT
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25-AUG-2000; 2000US-227961P
                          27-AUG-2001; 2001WO-US26738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phi C31 integrase; recombinase; transgenic; plant; agricultural food product; self-excising polynucleotide; plasmid; ds; pBPS EW051; T-DNA; cyclic; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= g7pA
2288..519
                                                                                                                                                                      9735..9880
                                                                                                                                                                                                                            /label= Nopaline_synthase_terminator 9690..9728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "1485..273
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3..217
                                                                                                                                                                                                                                                                       9411..9677
                                                                                                                                           function=
                                                                                                                                                                                 'label= attP
'note= "Recombinase target site"
                                                                                                                                                                                                                                                                                    /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product=
                                                                                                                                                                                                                                                                                                                                                                                                          product= "Phi_C31_intINT"
note= "Novel phi C31 integrase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Nopaline_synthase_terminator
1597..4933
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/label=_Nopaline_synthase_promoter
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977..7007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Octopine_synthase_promoter
260..4267
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                                                                                                         "The right T-DNA border and the left T-DNA border represent the end of the self-exclsing polynucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The left T-DNA border and the right T-DNA border represent the end of the self-excising polynucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target site"
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ABK12557;

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Matches 2021;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BADI )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New self-excising polynucleotides, useful for producing transplants, removing transgenes from these plants or crops (e.g. plants, removing transgenes from these plants or crops (e.g. plants, removing transgenes from the distribution of transgenes controller.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example
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                                                     GACGTGTCGCGCTTCTCGCGCCCTGAAGGTCATGGACGCGATTCCGGATTGTCTCGGAATTG
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                                        GACGTGTCGCGCTTCTCGCGCCTGAAGGTCATGGACGCGATTCCGATTGTCTCGGAATTG
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integrase; C31-Int mediated inversion; ds.
                       ARTEMIS PHARM GMBH.
FRANKGEN BIOTECHNOLOGIE
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Cytomegalovirus.
Unidentified.
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inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional orientation of the gene to be trapped. The cell comprising the gene trapping construct is useful for the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is useful to study gene function at various developmental stages. The gene genes. The present is useful for mutationally inactivating all cellular vector is transfected into a murine cell along with the test vector pRK65 is used for the expression of phiC31 integrase to detect C31-Int (a phiC31 phage derived integrase) mediated inversion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition seems (RRSS) specific to site specific recombinase which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates which is capable of uncess (RRSS) specific to site specific recombinates (RRSS) specific recombinates (
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Query Match
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Matches 1805; Conserv 1181 11211001 1061 393 333 273 GTCGGCGTTCGGGACGGCGGAGCGCCCGGAGTTCGAACGCATCCTGAACGAATGCCGCGC GTCGGCGTTCGGGACGGCGGAGCGCCCCGGAGTTCGAACGCATCCTGAACGAATGCCGCGC AGTCGAGCGCGACGGGGCCGGGTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCGGGCAC AGTCGAGCGCGACGGGGCCCGGTTCAGGTTCGTCGGGCATTTCAGCGAAGCGCCGGGCAC AGCAAGCCCAGCGACACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA 332 Conservative 88.5%; 0; Mismatches Score 1796.6; Pred. No. 0; DB 22; 14; Indels Length 5711; 0 Gaps 1180 1240 452 392 1060 272

Sequence 5711 BP; 1329 A; 1512 C; 1616 G; 1254 T; 0 other;

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CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGATTCTCGACACGAAGAACCTTCA

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GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA

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                                                         CC recombinases. The method comprises transforming cells with a first CC plasmid comprising two recombination sites and a coding sequence of cc interest, and a second plasmid encoding an altered recombinase; allowing recombination of the two recombination sites using the altered recombinase; screening and isolating transformed cells comprising the CC recombinase; The altered recombinase is useful for site-specifically critically a polynucleotide sequence of interest in a genome of a cell. CI is also useful in genetic engineering of chromosomes of higher cells. CC and for the generation of transgenic cells, tissues, plants and animals. CC e.g. ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia, chronic granulomatous disease, buchenne's muscular dystrophy, hammophilia, Fanconi's disease, sickle-cell anemia, Gaucher's disease, finited severe combined immunodeficiency (SCID), infectious diseases including viral and bacterial infections, acquired clicorders including viral and bacterial infections, acquired clicorders including viral and bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinase; genetic engineering; monogenic disorder; ADA deficienc cystic fibrosis; familial-hypercholesterolaemia; haemophilia; chronic granulomatous disease; Duchenne's muscular dystrophy; Fanconi's disease; anemia; sickle-cell anemia; Gaucher's disease; Hunter's syndrome; X-linked severe combined immunodeficiency; SCID;
            disorders including solid tumours and haematopoietic cancers such leukaemias and lymphomas, and other cancers. The present sequence encodes a wild type bacteriophage thetaC31 integrase.
                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying altered recombinase, involves hybridizing recombination sites in cells having specific coding sequence, transformed with altered recombinase gene, and isolating cells having product of the
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                                                               GATCGTTGTCACGAAGTCGACTACGGGCAGGGGCAGGGAACGCCCATCGAGAAGCGCGC
                                                                                                  GCTTCCCCTTGACCAATGGTTCCCCGAAGACGCCGACGCTGACCCGACCGGCCCTAAGTC
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AAQ06904 AAQ06904; standard; DNA;

3401

AAQO590

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06-MAR-1991

Sequence encoding phage phi C31. site specific integrating function of. actimomycete

Antibiotic production; isovaleryl; spiramycin;

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Best Local Similarity
Matches 1803; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence may be incorporated into a plasmid with an antibiotic biosynthetic gene (eg. isovaleryl or spyramycin) and used to transform a microorganism with site specific integration. Plasmids pKC796, pOJ243, pSKC50 and pSK51 and actimomycetes transformed by them, are specifically claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Use of site-specific integrating function of phage 0C31 - for increased prodn. of antibiotics and prodn. of hybrid antibiotics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-377895/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 4-6; 46pp; English.
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813 CTCGACCACTCCCCTTACCGGACCCTTCGAGTTCGAGCCCGACGTAATCCGGTGGTGGTG 872
                      GCGCGAATTGGGCGGGTACGTCGGCGGGAAGGCGCCTTACGGCTTCGAGCTTGTTTCGGA 752
                                                                                                                                                                                                                                                                          AGTCGAGCGCGACGGGGCCGGTTCAGGTTCGTCGGCCATTTCAGCGAAGCGCCGGCCAC 392
                                                                                                                                      CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGAATTCTCGACACGAAGAACCTTCA 692
                                                                                                                                                                                        GGAAGGCGTCTTCCGGCAGGGAAACGTCATGGACCTGATTCACCTGATTATGCGGCTCGA 632
                                                                                                                                                                                                                                        GGACGCGATTCCGATTGTCTCGGAATTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCA 572
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                                                                                                                                                                         GGAAGGCGTCTTCCGGCAGGGAAACGTCATGGACCTGATTCACCTGATTATGCGGCTCGA
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                                                                                                                         CGCGTCGCACAAAGAATCTTCGCTGAAGTCGGCGAAGATTCTCGACACGAAGAACCTTCA 1011
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GATCGTTGTCACGAAGTCGACTACGGGCAGGGGAGGGAACGCCCATCGAGAAGCGCGC 19	TGGTGGGGGCGCGCGTCAGTAGACGACAAGCGCGTGTTCGTCGGGCTCTTCGTAGAC	GTGGGGGCGCGCGTCAGTAGACGACAAGCGCGTGTTCGTCGGCCTCTTTCGTAGA	GTTGCCCCTTGACCAATGGTTCCCCGAAGACGCCGACGCTGACCCGACCGGCCCTAAGTC 18	CTCCGGCAGCAAGGGGCGGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGA	GCTCCGGCAGCAAGGGGGCGGAAGAGGCGGCGTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA 17	AGGCGCGTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCTGAC 20	GAGCTTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCT	TGTTGCGGAGCGCCGACGCCCTGAACGCCCTTGAAGAGCTGTACGAAGACCGCGGGC 19	GTTGCGGAGCGCCGACGCCCTGAACGCCCTTGAAGAGCTGTACGAAGACCGCGCGG	CGCCCGACGCTTCGGCAAGCTCACTGAGGAGGCGCCTGAGAAGAGCGGCGAACGGGCGAACCT 19	осссвасвсттсвеславстсастваевсесстваелаваевсеведализевесвалсс	CTTCAACAAGATCAGGCACGCCGAAGGCGACGAAGAGACGTTGGCGCTTCTGTGGGAAGC 18	TTCAACAAGATCAGGCACGCCGAAGGCGACGAAGAGACGTTGGCGCTTCTGTGGGAAG	GCACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCAT 17	CACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCA	GATCAAGGACTCTTACCGCTGCCGTCGCCGGAAGGTGGTCGACCCGTCCGCACCTGGGCA 17	ATCAAGGACTCTTACCGCTGCCGTCGCCGGAAGGTGGTCGACCCGTCCGCACCTGGGC	CATGGACAAGCTGTACTGCGAGTGTGGCGCCGTCATGACTTCGAAGCGCGGGGAAGAATC 16	ATGGACAAGCTGTACTGCGAGTGTGGCGCCCGTCATGACTTCGAAGCGCGGGGAAGAAT		TGGTTGGACGGCAGGGGGCGCGCGAAGGGGCTTTCCCCGGGGGCAAGCCATTCTGTCCG	GCCGGTCGAGCTTGATTGCGGACCGATCATCGAGCCCGCTGAGTGGTATGAGCTTCAGGC 15	CCGGTCGAGCTTGATTGCGGACCGATCATCGAGCCCGCTGAGTGGTATGAGCTTCAGG	CGGCACGCCGACCACGAAGATTGAGGGTTACCGCATTCAGGCGCGACCCGATCAGGCTCAGCTCCG 11 [CTTCGGGACCCGCGTATTGCGGGCTTCGCCGCTGAGGTGATCTACAAGAAGAAGCCGGA I	CCTTCGGGACCCGCGTATTGCGGGCTTCGCCGCTGAGGTGATCTACAAGAAGAAGAAGCAGA 111	GAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCG	CGAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCGAAT 10	CCCGGCCAGCATCACGGGGCTTTGTAAGCGCATGGACGCTGACGCCGTGCCGACCCCGGGG 13	CCGGGCAGCATCACGGGGCTTTGTAAGCGCATGGACGCTGACGCCGTGCCGACCCGGG	GCGTGAGATCAAGACGCACAAACACCTTCCCTTCAAGCCGGCAGTCAAGCCGCCATTCA 12	CGTGAGATCAAGACGCACAAACACCTTCCCTTCAAGCCGGGCAGTCAAGCCGCCATTC		
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              recombinases. The method comprises transforming cells with a first plasmid comprising two recombination sites and a coding sequence of interest, and a second plasmid encoding an altered recombinase; allowing recombination of the two recombination sites using the altered recombinase; screening and isolating transformed cells comprising the product of the sequence of interest; and identifying the altered recombinase. The altered recombinase is useful for site-specifically integrating a polynucleotide sequence of interest in a genome of a cell. It is also useful in genetic engineering of chromosomes of higher cells, and for the generation of transgenic cells, tissues, plants and animals. The altered recombinase is useful for treating monogenic disorders, e.g. AbA deficiency, cystic fibrosis, familial-hypercholesterolaemia, anemia, chronic granulomatous disease, Duchenne's muscular dystrophy, anemia, chronic granulomatous disease, Duchenne's muscular dystrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying altered recombinase, involves hybridizing recombination sites in cells having specific coding sequence, transformed with stered recombinase gene, and isolating cells having product of the
                                                                                                                                                                                                                                                                                                                                                                                  The specification
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        sickle-cell
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combined immunodeficiency;
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dystrophy,
c's disease
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Best Local S
Matches 1801
   1113
                                                    1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunter's syndrome and X-linked severe combined immunodeficiency (SCID), infectious diseases including viral and bacterial infections, acquired disorders including solid tumours and haematopoietic cancers such as leukaemias and lymphomas, and other cancers. The present sequence encodes an altered recombinase of the invention.
                            864
                                                                             804
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CGGCACGCCGACCACGAAGATTGAGGGTTACCGCATTCAGCGCGACCCGATCACGCTCCG
                                    CCTTCGGGACCCGCGTATTGCGGGCTTCGCCGCTGAGGTGATCTACAAGAAGAAGCCGGA
                                                                                      CGAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCGAAT
                                                                                                                        CCCGGGCAGCATCACGGGGCTTTGTAAGCGCATGGACGCTGACGCCGTGCCGACCCGGGG
                                                                                                                                       CCCGGGCAGCATCACGGGGCTTTGTAAGCGCATGGACGCCTGACGCCGTGCCGACCCGGGG
                                                                                                                                                                                                                                     CTCGACCACTCCCCTTACCGGACCCTTCGAGTTCGAGCCCGACGTAATCCGGTGGTGGTG
                                                                                                                                                                                                                                                                         GACGAAGGAGATCACGCGCAACGGCCGAATGGTCAATGTCGTCATCAACAAGCTTGCGCA
                                                                                                                                                                                                                                                                                      GACGAAGGAGATCACGCGCAACGGCCGAATGGTCAATGTCGTCATCAACAAGTTAGCGCA
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                                                                         CGAGACGATTGGGAAGAAGACCGCTTCAAGCGCCTGGGACCCGGCAACCGTTATGCGAAT
                                                                                                                                                                                                                           CTCGACCACTCCCCTTACCGGACCCTTCGAGTTCGAGCCCGACGTAATCCGGTGGTGGTG
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Nucleotide sequence of altered recombinase
                 29-OCT-2001
                                   AAH74881;
                                                     AAH74881 standard;
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Recombinase; genetic engineering; monogenic disorder; ADA deficiency; cystic fibrosis; familial-hypercholesterolaemia; haemophilia; chronic granulomatous disease; Duchenne's muscular dystrophy; Fanconi's disease; anemia; sickle-cell anemia; Gaucher's disease; Hunter's syndrome; x-linked severe combined immunodeficiency; SCID; infectious disease; acquired disorder; tumour; cancer; ss.

Synthetic.
Bacteriophage

Key

Location/Qualifiers
CDS

/*tag= a
/product= "altered recombinase 5c1"
/note= "no termination codon given"

WO200161049-A1.

23-AUG-2001; 2001WO-US05269.
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Identifying altered recombinase, involves hybridizing recombination sites in cells having specific coding sequence, transformed with altered recombinase gene, and isolating cells having product of the sequence -

P-PSDB;

2001-522610/57

MP, SO

[V LELAND Sclimenti

CR;

STANFORD

JUNIOR

Disclosure; Fig 8; 101pp; English.

CC The specification describes a method for identifying altered combinases. The method comprises transforming cells with a first CC plasmid comprising two recombination sites and a coding sequence of interest, and a second plasmid encoding an altered recombinase; allowing crecombination of the two recombination sites using the altered cc product of the sequence of interest; and identifying the altered cc product of the sequence of interest; and identifying the altered cc product of the sequence of interest; and identifying the altered cc product of the sequence of interest; and identifying the altered cc product of the sequence of interest in a genome of a cell. It is also useful in genetic engineering of chromosomes of higher cells, and for the generation of transgenic cells, tissues, plants and animals. CC e.g. ADA deficiency, cystic fibrosis, familial-hypercholesterolaemia, canemia, chronic granulomatous disease, Duchenne's muscular dystrophy, haemophilia, Fanconi's disease, sickle-cell anemia, Gaucher's siseases, cluders's syndrome and X-linked severe combined immunodeficiency (SCID), confectious diseases including viral and bacterial infections, acquired clisvaters and lymphomas, and other cancers. The present sequence cc encodes an altered recombinase of the invention.

Sequence 1839 BP; 388 A; 547 C; 613 G; 291 T; 0 other;

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γ
                    В
                                  δÃ
                                                   Query Match 87.9
Best Local Similarity 99.0
Matches 1797; Conservative
       273
                     24
                    AGCAAGCCCAGCGACACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA
                                                           87.9%;
99.0%;
                                                    0;
                                                    Score 1785.6;
Pred. No. 0;
0; Mismatches
                                                                    DВ
                                                     19;
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                                                     Indels
                                                                    Length
                                                                    1839;
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84

AGCAAGCCCAGCGACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA

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                WO200161049-A1
                                                                                                                                    Recombinase; gene cystic fibrosis;
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                                                                                                                                                                   CTTCAACAAGATCAGGCACGCCGAAGGCGACGAAGAGACGTTGGCGCTTCTGTGGGAAGC
                                                                                                                                                                                                                      GCACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCAT
                                                                                                                                                                                                                                                                        GATCAAGGACTCTTACCGCTGCCGTCGCCGAAGGTGGTCGACCCGTCCGCACCTGGGCA
                                                                                                                                                                                                                                                                                                                            CGGCACGCCGACCAAGATTGAGGGTTACCGCATTCAGCGCGACCCGATCACGCTCCG
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                         AGGAGCTTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCGTGAC
                                                                            TGTTGCGGAGCGCCGACGCCCTGAACGCCCTTGAAGAGCTGTACGAAGACCGCGCGC
                                                                                                                              CGCCCGACGCTTCGGCAAGCTCACTGAGGCGCCTGAGAAGAGCGGCGAACGGGCGAACCT
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                                                                                                                  CGCCCGACGCTTCGGCAAGCTCACTGAGGCGCCTGAGAAGAGCGGCGAACGGGCGAACCT
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563 812 623 872

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1103 1352 1163 1232

1043 1292 1172

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1472 1283 1532

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RESULT 10
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ID AAD19829
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XX AAD19
XX AAD19
XX AAD19
XX 18-DE
CEST
KW Cestr
KW Cestr
KW Castr
FT intro
FT intro
FT intro
FT intro
FT Visa
XX W2000
XX W2000
XX W2000
XX W21;
XX WPI;
XX Castr
PT Novel
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CC The i
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CC Capre
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28-APR-2000;
26-JAN-2001;
                                                                                                                       Novel
virus
polynucleotide sequence. These CmYLCV DNA molecuexpression of associated polynucleotide sequence relates to recombinant DNA sequences containing
                                                                                                                                                                                                                                                                                                                                                                                        Key
intron
                                                                                Example
                                                                                                           polynucleotide
                                                                                                                                                                                                                                                                                       26-MAR-2001;
                                                                                                                                                                                                                                                                                                               04-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                          Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cestrum yellow leaf curl transgenic plant; green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green
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         invention relates to Cestrum yellow leaf curling virus (CMYLCV) novel sequences which functions as transcription promoters of an associated ynucleotide sequence. These CMYLCV DNA molecules confers constitutive ression of associated polynucleotide sequences. The invention also
                                                                                                                                                                                     Ŧ,
                                                                                                                                                            2001-616524/71.
                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAGACGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAAGACGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCGGCAGCAAGGGGCGGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fluorescent
                                                                               19; Page 66;
                                                                                                                                                                                                          SYNGENTA PARTICIPATIONS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberosum
                                                                                                                                                                                  Stavolone L,
                                                                                                            sequence obtained from of conferring constitutive otide  -
                                                                                                                                                                                                                                   2000GB-0007427.
2000GB-0010486.
2001EP-0101802.
                                                                                                                                                                                                                                                                                      2001WO-EP03408
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           curling
                                                                            100pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                            "Solanum tuberosum
                                                                                                                                                                                    De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              912
                                                                                                                                                                                                                                                                                                                                                                                                                                                             fluorescent protein 1;
                                                                                                                                                                                  Haan
                                                                            English
                                                                                                                                from genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virus; CmYLCV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synGFP1 gene with ST-LS1 intron
                                                                                                                                                                                  PΤ,
                                                                                                                   genome of Cestrum expression of an
                                                                                                                                                                                  Ligon
                                                                                                                                                                                  HT,
                                                                                                                                                                                                                                                                                                                                                             ST-LS1
                                                                                                                                                                                  Kononova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFP1;
  promoter
                                                                                                                                                                                                                                                                                                                                                             .intron"
                                                                                                                   yellow leaf curling associated desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds
                                                                                                                                                                                  ×
  sequences
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RESULT 11
AAD19834
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Best Local s
Matches 204
                                                                                                                                                                                                                                                transgenic plant GFP1; ds.
                                               27-MAR-2000;
28-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                                       Chimeric
Chimeric
Chimeric
WPI; 2001-616524/71
                 Hohn
                                                                                                  04-OCT-2001
                                                                                                                                                                        misc_feature
                               (SYGN)
                                                                                26-MAR-2001;
                                                                                                                                                                                                promoter
                                                                                                                                                                                                         Key
                                                                                                                 WO200173087-A1
                                                                                                                                                  terminator
                                                                                                                                                                                                                                                                                      Promoter-reporter cassette
                                                                                                                                                                                                                                                                                                      18-DEC-2001
                                                                                                                                                                                                                                                                                                                       AAD19834
                                                                                                                                                                                                                                                                                                                                      AAD19834 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are used for creating transgenic plants expressing DNA of interestimes and in most tissues and organs. The present DNA sequence is fluorescent protein-1, synGFP1 gene with ST-LS1 intron sequence. optimised GFP reporter gene is used in the construction of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local 204;
                                                                                                                                                                                                                                                                                                                                                                             445 CCAAAATTTGTTGATGTGCAGGTGCAGGAGCGC
                                                                                                                                                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                                                                                                                                              385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ,
                                                                                                                                                                                                                                                                                                                                                                                            CCAAAATTTGTTGATGTGCAGGTACGCGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                          TTAGTAGTAATATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAGTAGTAATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCA
                               SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
              Stavolone
                                                                                                                                                                                                                          ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             912 BP;
                                                                                                                                                                                                                                                             llow leaf curling virus; Cn plant; nopaline synthase;
                                              ; 2000GB-0007427.
; 2000GB-0010486.
; 2001EP-0101802.
                                                                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                              Cestrum yellow leaf curling Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                2001WO-EP03408
                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                        /note= "CmYLCV CmpC 380..1292
                                                                                                                                                                                                Location/Qualifiers
1..354 `
                                                                                                                                /*tag=
/note=
                                                                                                                                                 /note= "Corresponds
1304..1577
                                                                                                                                                                                        /*tag=
                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 A; 245 C;
               ŗ
                                                                                                                                                                                                                                                                                                                                      DNA; 1577
                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.8%;
               De
                                                                                                                                "Nopaline
               Haan
                                                                                                                                                                                                                                                                                      #
3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
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               PT,
                               ĀG
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                                                                                                                                synthase
                                                                                                                                                                                                                                                                                     construct plant
                                                                                                                                                                                                                                                              cmYLCV; transcription;
e; NOS; green fluoresce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 4.8e-35
               Ligon
                                                                                                                                                        ť
                                                                                                                                                                                promoter
                                                                                                                                                                                                                                      virus
                                                                                                                                                        SynGFP1
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                                                                                                                                                                                                                                                                                                                                                                                            233
               HT,
                                                                                                                                                                                                                                                             green
                                                                                                                                (NOS)
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                                                                                                                                                                               fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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               Kononova
                                                                                                                               terminator"
                                                                                                                                                                                                                                                           fluorescent
                                                                                                                                                                                                                                                                                    transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           912;
                                                                                                                                                                                                                                                             protein-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is
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RESULT 12
AAD19832
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AAD19832
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AAD19
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AAD19
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Best Local
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                                                                                                                                                                                                                                                                                                                                                              Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which are used for creating transgenic plants expressing DNA of interest at all times and in most tissues and organs. The present DNA sequence is a promoter-reporter cassette which contains CmYLCV CmpC promoter fragment, green fluorescent protein-1 synGFP1 reporter gene and the Agrobacterium tumefaciens nopaline synthase (NOS) terminator. Promoter-
                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic
GFP1; ds.
                           WO200173087-A1
                                                                                                                         terminator
                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                            Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cestrum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter-reporter cassette #1 to construct plant transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reporter cassette is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 19; Page 72-73; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide
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for conferring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yellow
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                                                                                                                                                                                                                                                                                                                                       Cestrum yellow leaf curling Agrobacterium tumefaciens. Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leaf curling
                                                                                                                                                                                               /note- "CmYLCV CmpS 411..1331
                                                                                                                      /note= "Corresponds
1343..1618
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                      /*tag-
                                                                                                                                                                                                                                            /*tag-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%;
95.8%;
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                                                                      "Nopaline synthase (NOS) terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to construct plant transformation vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 198.6;
Pred. No. 5.9e
0; Mismatches
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                                                                                                                                                                                                                   promoter fragment"
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                                                                                                                                             SynGFP1 gene'
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5.9e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-1;
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Matches 204
           Chimeric - Chimeric - Chimeric - 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which are used for creating transgenic plants expressing DNA of interest at all times and in most tissues and organs. The present DNA sequence is a promoter-reporter cassette which contains CnYLCV CmpS promoter fragment, green fluorescent protein-1 synGFP1 reporter gene and the Agrobacterium tumefaciens nopaline synthase (NOS) terminator. Promoter-reporter cassette is used to construct plant transformation vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel
virus
                                                                     Cestrum yellow leaf curling virus; CmYLCV; transcription; maize; transgenic plant; nopaline synthase; NOS; green fluorescent prot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hohn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to Cestrum yellow leaf curling virus (CmYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CmYLCV DNA molecules confers constitutive
                                                                                                          Ubq3(At)-synGFP1-NOS terminator expression
                                                                                                                                  18-DEC-2001
                                                                                                                                                          AAD19840;
                                                                                                                                                                                  AAD19840 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1618 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 19; Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polynucleotide
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26-JAN-2001;
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                                                                                                                                                                                                                                                                                             ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                          204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence obtained from genome of Cestrum yellow leaf curling conferring constitutive expression of an associaced desired
            Arabidopsis thaliana. Agrobacterium tumefaciens Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000GB-0007427.
2000GB-0010486.
2001EP-0101802.
                                                                                                                                  (first entry)
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                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 383 C; 400 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                              896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367 T; 0 other;
                                                                                                                                                                                                                                                                     233
                                                                        green fluorescent protein;
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RESULT 14
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                                                                                                                                                                                                                                                                                                        Ubd3(At)-synGFP1-NOS terminator expression cassette which comprises Arabidopsis thaliana ubiquitin 3 promoter, Ubd3(At) operatively link with green fluorescent protein-1, synGFP1 reporter gene and Agrobacterium tumetaciens nopaline synthase (NOS) terminator. This expression cassette is used for the construction of plant transform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-2000;
28-APR-2000;
26-JAN-2001;
                                                                                          2131
                                                                                                                                        2071
                                                                                                                                                                                     2011
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to Cestrum yellow leaf curling virus (CMYLCV) novel DNA sequences which functions as transcription promoters of an associated polynucleotide sequence. These CMYLCV DNA molecules confers constitutive expression of associated polynucleotide sequences. The invention also relates to recombinant DNA sequences containing promoter sequences which
                                                                                                                                                                                                                                                                               Sequence 2943 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel DNA sequence obtained from genome of Cestrum
                                                                                                                                                                                                                                                                                                                                                                                    are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS
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                                                                                                                                                                                                           21
                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                 used for creating transgenic plants expressing DNA of interest es and in most tissues and organs. The present DNA sequence is a
                                                                                                   TTAGTAGTAATATATATTTCAAATATTTTTTCAAAATAAAAAGAATGTAGTATATAGCA 140
                                                                                                                                                                                              CCAAAATTTGTTGATGTGCAGGTGCAGGAGCGC
                                                                CCAAAATTTGTTGATGTGCAGGTACGCGGGTGC
                                                                                    ATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTTTATAACTTTTCTAATATATGA
                                                                                                                                   TTAGTAGTAATATATTTCAAATATTTTTTTCAAAATAAAGAATGTAGTATATAGCA
                                                                                                                                                                               Ţ,
                                                                                                                                                                                                                                 204;
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 2000GB-0007427.
; 2000GB-0010486.
; 2001EP-0101802.
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/note= "Arabidopsis ubiquitin 3
1738..2658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene"
2670..2943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note- "Nopaline synthase (NOS) terminator"
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                                                                                                                                                                                                                                                                           886 A; 544 C;
                                                                                                                                                                                                                                         9.8%;
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Pred. No. 7.5e
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                                                                                                                                                                                                                                                                           929.T; 0 other;
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/.5e-35;
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                                                                                                                                                                                                                              Indels
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associated d
                                                                                                                                                                                                                                                    2943;
                                                                                                                                                                                                                                                                                                             transformation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-2000;
28-APR-2000;
26-JAN-2001;
                                                                                                                                                                                                               Sequence 2001 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hohn
                                                                                                                                                                                                                                                                                                                                                                                           Novel DNA sequence obtained from genome of Cestrum yellow leaf curling virus for conferring constitutive expression of an associated desired polynucleotide
  210
                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 67-68; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SYGN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2001
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                                               150
                                                                                                                     383
                                                                                              90
                                                                                                                           plant
GTTGATGTGCAGGTA 224
                                                                  CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT
                                   CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT 209
                                                                                          ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-616524/71
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                      (GUS reporter gene with intron) gene transformation vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stavolone L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant;
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; 2000GB-0007427.
; 2000GB-0010486.
; 2001EP-0101802.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-EP03408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leaf curling virus; CmYLCV;
nt; beta-glucuronidase; GUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 385..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                              532 A; 451 C; 535 G; 483 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GUS) reporter gene with ST-LS1 intron sequence
                                                                                                                                                                                         9.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Haan PT,
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Pred. No.
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                                                                                                                                                                             4.2e-34;
                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ST-LS1 intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription;
                                                                                                                                                                                                                                                 is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kononova
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GTTGATGTGCAGGTA

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RESULT 15
ABK15667
targeting an associated protein of interest to plastids. A nucleic acid which expresses polypeptide having ilpoxygenase activity is useful for inhibiting fungal mycotoxins when transformed into a plant. The lipoxygenase is useful for inhibiting fungal mycotoxins. The promoter is useful for regulating transcription of a chemically inducible but not wound or pathogen inducible gene, which involves applying a chemical regulator to a plant or seed containing a chemically regulatable nucleotide sequence. Transgenic plants as described above are useful for preeding improved plant lines that for example increase the effectiveness of conventional methods such as herbicide or pesticide treatment or allow to dispense with improved stress tolerance can be obtained that, due to their optimised genetic equipment yield harvested product of better contails.
                                                                                                                  quality than products that were not able to tolerate comparable adverse developmental conditions. The present sequence is the glutathione-Stransferase (GUS) sequence (containing an intron from solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding a promoter which is capable of driving chemically inducible but not wound- or pathogen-inducible expression of an associated nucleotide sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; lipoxygenase; RCI-1; transgeni rice chemically induced cDNA; prom fungal mycotoxin inhibitor; plant GUS; GIG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               comprising the promoter or fragments and a transgenic plant comprising the vector. The promoter or fragments are useful for expressing a nucleotide sequence of interest. The transit peptide is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducible expression of an associated nucleotide sequence. Also included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone for the lipoxygenase gene, promoter fragments, the lipoxygenase transit peptide which directs expressed proteins to the plastid, a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule (a promoter of rice chemically induced cDNA (RCI-1), which encodes a lipoxygenase) capable of driving chemically-inducible that the wound- or pathogen-inducible of the control of the capable of the control of the control of the control of the control of the capable of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 17; Page 75; 88pp; English.
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15-SEP-2000;
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Chimeric - Solanum tuberosum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2002
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                                                           lipoxygenase promoter regions in a vector construct.
                                                                                                 tuberosum, referred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-188550/24
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2000GB-0022739
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induced cDNA; promoter; transit peptide; plastid
                                                                                          to as GIG) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawton KA;
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Sequence 2001 BP;

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Pred. No. 4.2e-34;
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Search completed: May 11, 2003, 18:05:27 Job time: 535.5 secs

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AL301578
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EST557172
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EST619984
Tetraodon
Drosophil
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AUTHORS
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                                                                                                                                                                                     potato.

Solanum tuberosum

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 675)

van der Hoeven, R., Sun, H., Karamycheva, S.A., Tsai, J., Van Aken, S.,

Utterback, T., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C.,

Utterback, T., and Baker, B.
                                                                                                                                                                                                                                                                                                                                                                                BM109636
EST557172 potato :
mRNA sequence.
BM109636
                                                         Tanksley, S. and Baker, B.

Generation of ESTs from potato roots
Unpublished (2001)
Contact: Research Genetics, Libraries Division
Tel: 1-800-711-6195
Email: cdna@resgen.com
For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                EST
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/cultivar="Kennebec"
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                                                 Location/Qualifiers
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AL062360 Drosophil
B96681 T3001TR TAM
AQ286687 RPCI11-81
AL053529 Drosophil
BQ596436 PfESTOAb3
AL087992 Arabidops
BH438258 BOGL267TF
BH178455 011____02-
AL615412 T3 end of
AL106896 Drosophil
AQ583787 RPCI-11-4
AL075293 Drosophil
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167; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Email: potato@tigr.org
This clone is available through the Research Genetics, cc
Research Genetics for further information 1-800-711-6195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Other_ESTs: EST619984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buell, C.R., Hart, A., Baker, B., Restrepo, S., Griffiths, H., van Karamycheva, S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                    cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robin Buell
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12 Medical Center Dr, Rockville,
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/clone_lib-"Generation of a set of potato cDNA clones microarray analyses mixed potato tissues" \,
                                                                                                                     /cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
                                                                                             /clone="STMHZ22"
                                                                                                                                                                                               /organism="Solanum tuberosum"
                                                                                                                                                                                                                                              . .804
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                                                                                                                                                                                                                                                                             ocation/Qualifiers
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/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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/clone="cPRO4H6"
/clone_lib="potato roots"
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The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2002)
Other_ESTs: EST619983
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BO512569
EST61958 deneration of a set analyses mixed potato tissues
3'_end, mRNA sequence.
                                                                                                                                                                                                                                                                     cdna@resgen.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                      This clone is available through the Research Genetics, contact the Research Genetics for further information 1-800-711-6195 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karamycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses
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                                                                                                                                                                                                                                                                                                                                                  potatoetigr.org
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhOI; supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
                                                            /clone_lib="Generation of a set of potato cDNA clones microarraye analyses mixed potato tissues" /tissue_type="mixed tissues" /lab_host="SOLR"
                                                                                                                                                                 /cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
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/lab_host="SOLR"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets.
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Pred. No. 3.4
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a set of potato cDNA clones
ssues Solanum tuberosum cDNP
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der Hoeven,R., Tsai,J. and
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167; Conserv
                                                                                                                                                                                                                       This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bouneau, L., Billault, A., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier Saurin, W. and Weissenbach, J.
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127N16 of
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                                                                                                                                                                                                                                                                                                                                                                                   Genoscope.
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Tetraodon nigroviridis.
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Pred. No. 3.4e-18;
""" here's 27;
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Quetier,F., Saurin,W., Bernot,
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Drosophila melanogaster genome survey sequence T7 end of I
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                              at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/organism="Drosophila
/db_xref="taxon:7227"
/clone="BACR27A24"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by 
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Ephydroidea; Drosophilidae; Drosophila.
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/note="end : SP6"
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Drosophila melanogaster genome su
BACN17H15 of DrosBAC library from
          fly), genomic survey sequence.
AL107447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid
Seq primer: TF
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Tel: 301-838-3523
Fax: 301-838-0208
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/strain="T01000H3"
/db_xref="taxon:3712"
/clone="BOGSL20"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                          Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a Mi
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/clone_lib="DrosBAC"
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/db_xref-"taxon:7227"
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Arabidopsis thaliana

AL089326.1 AL089326 survey sequence

GI:5290466

Arabidopsis thaliana genome survey sequence TAMU library from strain Columbia of Arabido

780 bp

DNA

linear

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                                                                                                                                                                                                                                                                                                                            GAGGGSGRGGGSGCCASSGVCGAACSSASCSSASMCGVSSGSSCSASCGSCCGVSSCSAV
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                                                                                                                                                             TTGCTCGCCCTGGGCGTGACGATTGTTTCCACTCAGGAAGGCGTCTTCCGGCAGGGAAAC
                                                                                                                                                                                                                                                                                             CMAADCGGCCAKMACCSSSSASSSGSSCASTSSSASRGGMVSSCACSGSGSGGASACGAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATACAAAAAAATTTAAAAATAARAAGTATWATAWAATWWAGNATTAWATNTWNTNAANN 518
                                AAGTCGGCGAAGATTCTCGACACGAAGA
                                                                                              GTCATGGACCTGATTCACCTGATTATGCGGCTCGACGCGTCGCACAAAGAATCTTCGCTG
                                                                                                                                                                                               TATGACGTGTCGCGCTTCTCGCGCCCTGAAGGTCATGGACGCGATTCCGATTGTCTCGGAA 537
                                                                                                                                                                                                                                                                SASSASSVMSKVASAVASCSAVASGMSAGAVSSSCRSSVASSVSAAASVSSSVSSSSSSS
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VASASASASVSSVAAAVAAAMAAAAASA 1086
                                                             SASSYSSSSSSSTSSSASYSSYSAYSMSAYVSSSASSSSSYSYSSYVAVAASAAAAAA
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/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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a 176 c 160 g
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/db_xref="taxon:7227"
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- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton oroject grant. The Nas been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAAGTGTGTATATTTAATTTAT 182
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Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                      Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence SP6 end of BAC BACN03017 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                 Direct Submission
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anoubat, M., Choisne, N., Artiguenave, F.,
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/strain="Columbia"
/strain="columbia"
/db_xref="taxon:3702"
/clone="T3K15"
/clone=lib="TAMU"
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     /organism="Drosophila
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                                                                                                                                                                                                                                          - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EBCEP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Biliaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN03017"
/clone=lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
a 158 c 150 g :
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                                                                              /plasmid="pBeloBAC11"
/note="end : SP6"
216 c 197 g
                                                                                                                         /clone="BACN01I20"
/clone_lib="DrosBAC"
                                                                                                                                                         /organism="Drosophila
/db_xref="taxon:7227"
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(E-mail : segref@genoscope.cns.f.
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                              DB 17;
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                                                         TTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTTCTGTAGTTTATAAGTGTG 167
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                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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153P04 of library
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Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                   /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="153P04"
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/note="Genoscope sequence ID : COAG153DH028P1~end
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                                                                                                                                                                                                Score 55.6; DB Pred. No. 0.044;
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AL053013
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                   Drosophila melanogaster genome sur
BACR19D16 of RPCI-98 library from
                                                                              CNS0091P
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/db_xref="taxon:7227"
/clone="BACR08K08"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's labbratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library. Or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information
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Direct Submission
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Ephydroidea; Drosophilidae; Drosophila
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-98-416-780

US-08-998-416-1011

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FILING DATE: 12-JUN-1989

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                                                                                                                                                                                                                      TELEFAX: (317) 231-7745
TELEFAX: (317) 231-743
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2633 bass --
Type:
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TOPOLOGY: line
MOLECULE TYPE: I
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,267
FILLING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
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CITY: Indianapolis
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                     MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                 NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCION NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
150 CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ramsay, Nicola
TITLE OF INVENTION: Method of Using Transactivation Proteins
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                   753
                                                                                                       693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                        ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT 149
                                         ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT
                                                                                            CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT 872
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11 South Meridian
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                     Score 195; DB 3;
Pred. No. 2.8e-38;
0; Mismatches 0;
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US-08-452-267-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 66
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
    868
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ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0,
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                            210
                                                         748 ATATAATATTTCAAATATTTTTTTCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTT
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FILING DATE: 26-MAY-1995
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                GTTGATGTGCAGGTA 224
                                              CTGTAGTTTATAAGTGTGTATATTTTAATTTATAACTTTTCTAATATATGACCAAAATTT
GTTGATGTGCAGGTA 882
                                                                                                                                                                                                         195;
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11 South Meridian
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Pred. No.
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RESULT 7
US-09-080-625-1
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Patent No. 6307123
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US-09-123-644-3
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US-09-123-644-3
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Best Local S
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INFORMATION FOR SEQ ID NO: ::
SEQUENCE CHARACTERISTICS:
LENGTH: 5534 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION: Method of Using Transactivation Proteins to
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                                                                                                                                   210 GTTGATGTGCAGGTA 224
                                                                                                                                                                              808 CTGTAGTTTATAAGTGTGTATATTTAAATTTATAACTTTTCTAATATATGACCAAAATTT
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REGISTRATION NUMBER: 38,833
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11 South Meridian
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SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                    Patent No. 643325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 197;
                             CURRENT APPLICATION NUMBER: US/09/695,782
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 09/080,625
PRIOR FILING DATE: 1998-05-18
                                                                                                  APPLICANT: GRIFFOR, MATTHEW TITLE OF INVENTION: METHODS / FILE REFERENCE: DEKM:161USC1
                                                                                                                                 APPLICANT: KRIZ, ALAN L. APPLICANT: GRIFFOR, MAT
NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn Ver.
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LENGTH: 1701 base pairs
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
TITLE OF INVENTION: IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/080,625 FILING DATE:
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                   AND COMPOSITIONS FOR TRANSGENE IDENTIFICATION
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Pred. No. 4e-38;
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; OTHER INFORMATION:
US-09-695-782-1
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 2, Application US/09080625 Patent No. 6307123
      Matches
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                                                                                                                TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                        TELEPHONE: (512) 418-3000
                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                               NAME: Hanson, Robert E.
REGISTRATION NUMBER: P-42,628
REFERENCE/DOCKET NUMBER: DEKM:161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203
                  Local
                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                              FILING DATE:
                                                                   TOPOLOGY:
                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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      197;
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197; Conserv
               Similarity
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                                                                                        nucleic acid
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                                                                                                    3336 base pairs
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     Conservative
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                                                                  linear
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Pred. No. 5.
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Pred. No. 4e-38;
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; OTHER INFORMATION:
US-09-695-782-2
                                                                                                                   US-09-080-625-4
                                                                                                                                    RESULT 11
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US-09-695-782-2
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                                                                     Sequence 4, Application Patent No. 6307123 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 3336
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Patent No. 6433
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CURRENT FILING DATE: 2000-10-24
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TRANSGENE
FILE REFERENCE: DEKM:161USC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
               APPLICANT: Kriz, Alan L. APPLICANT: Spencer, T. M. TITLE OF INVENTION: METH TITLE OF INVENTION: IDEN
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 SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer
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METHODS AND COMPOSITIONS IDENTIFICATION 19
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                                                                                                   US/09080625
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                           FOR TRANSGENE
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                                                                                                                                                                                                                                                                                                         Patent No. 6433252
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Best Local Similarity 97.5%;
Matches 197; Conservative
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                          APPLICANT: KRIZ, ALAN L.
APPLICANT: GRIFFOR, MATTHEW
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: DEKM:161USC1
CURRENT APPLICATION NUMBER: US/09/695,782
CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3877 base pairs
                                                                                                               SOFTWARE: PatentIn Ver. 2.0
                                                                                                                               NUMBER OF SEQ ID NOS: 19
                                                                                                                                              PRIOR APPLICATION NUMBER: 09/080,625 PRIOR FILING DATE: 1998-05-18
                                                          LENGTH: 38
OTHER INFORMATION: Description of Artificial Sequence:
                                          ORGANISM: Artificial Sequence
                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2042
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                   2162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                               ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
77210-4433
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STRANDEDNESS: double
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                                                                              3877
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Pred. No. 5.8e-38;
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RESULT 13
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SEQ ID NO 5
LENGTH: 5560
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1996-07-31
EARLIER APPLICATION NUMBER: EP 95401844.6
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEO ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/817,188 CURRENT FILING DATE: 1997-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: PCT/EP96/03366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENETIC TRANSFORMATION USING A PARP INHIBITOR FILE REFERENCE: 2121-0127P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DE BLOCK,
NAME/KEY: misc_feature
LOCATION: (2765)...(3058)
OTHER INFORMATION: 3' untranslated region of the CAM
OTHER INFORMATION: containing polyadenylation signals
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: (1)..(25) OTHER INFORMATION: RB:
                                                                                                                NAME/KEY: misc_feature
LOCATION: (830)..(2760)
OTHER INFORMATION: pSSU
                                                                                                                                                                                                                                                                               LOCATION: (84). (296)
OTHER INFORMATION: 3' 97: 3' untranslated
OTHER INFORMATION: polyadenylation signal
OTHER INFORMATION: T-DNA
                                                                                                                                                                                         OTHER INFORMATION: bar: region coding for phosphinotricin OTHER INFORMATION: acetyltransferase
                                                                                                                                                                                                        LOCATION: (318)..(869)
OTHER INFORMATION: bar
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of Arabidopsis thaliana
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Pred. No. 5.8e-38;
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FILE REFERENCE: ON CITCH OF TRANSGENIC PLANTS PRIOR APPLICATION MUMBER: US/09/367,293 PRIOR APPLICATION MUMBER: US/09/367,293 PRIOR APPLICATION NUMBER: PCT/GB98/00367 PRIOR APPLICATION NUMBER: PCT/GB98/00367 PRIOR APPLICATION NUMBER: GB 9702592.8 PRIOR FILING DATE: 1998-02-05 PRIOR FILING DATE: 1998-02-05	-2 Application US/09367293 (44878 RMATION: Donaldson, Lain A. Jorgensen, Kirsten Jorgensen, Kirsten Jorgensen, Kirsten	450 CTGTAGTTTAAAGTGTGTGTATATTTTAAATÄÄÄÄAGGATTGTTTT 4554 CTGTAGTTTATAAGTGTGTATATTTTTAAATÄÄÄÄÄÄÄÄÄÄ	TACGTAAGTTTCTGCTTCTACCTTTGATATATATATATAT	OTHER INFORMATION: (5475) US-08-817-188-5 Query Match Best Local Similarity 9.4%; Score 190.2. Matches 192; Consty 98.5%; Boore 190.2.	n unknown sequence (may) unknown sequence (may)	OTHER INFORMATION: (550) PEATURE INFORMATION: LB: left border sequence of octopine tocation: (5059) OTHER INFORMATION: TOTAL SEQUENCE of octopine tocation: (5059) OTHER INFORMATION: (5059) OTHER INFORMATION: region with	region coding region correspo rLS1 gene	fea 10N:
		TATGACCAAATGCTTTT 149 ATAGCAATTGCTTTT 455 TATGACCAAAATTGCTTTT 209 TATGACCAAAACAT 4495	h 5560; 0; Gaps 0; TTAGTAGTA 89 	ntain up to 20	up to	Ine TL-DNA from	for beta-glucuronidase	

COMPUTER 2000 COMPUTER 2000 MEDIUM TYPE: FLORPY disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE SOFTMARE: Patenth Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/487,826B APPLICATION NUMBER: US/08/487,826B APTORNEY AGENT INFORMATION: REGISTRATION NUMBER: 29,655 TELECOMMUNICATION NUMBER: NIHI21.001CP1 TELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: NIHI21.001CP1 TELECOMMUNICATION INFORMATION: REGISTRATION SOCIETY NUMBER: NIHI21.001CP1 TELECHONE: (619) 235-0350 INFORMATION FOR SOC ID NO.15 SEQUENCE CHARACTERISTICS LENGTH. 19124 base pairs	On US/08487826B L. Chetan Cohetan Louis H. David S. Phaun Phomas E. BINDING DOMAINS FROM PLASMODIUM VIVAX PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING Center Orive 16th Floor	TYPE: DA	R R C
	PROTEINS	Gaps 0, Gaps 0, HIA 92 HIA 294 WIA 294 WIA 294 F 212 F 212 F 414	Page
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Minimum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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      100%
                                             US-09-940-550A-11

US-09-788-297-20

US-09-788-297-26

US-09-788-297-27

US-09-788-297-28

US-09-887-576-582

US-09-887-576-581

US-09-969-373-1213

US-09-969-373-1213

US-09-969-373-1213

US-09-10-239-676-22

US-10-239-676-15

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US-10-239-676-15
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US-10-239-676-90
US-10-239-676-212
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US-09-940-550A-9
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9030.174 Million cell updates/sec
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                                             Sequence 27, Appl
Sequence 222, App
Sequence 8, Appli
Sequence 14, Appl
Sequence 117, Appl
Sequence 115, Appl
Sequence 1267, Ap
Sequence 90, Appl
Sequence 212, App
                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                    Sequence 27, Appl
Sequence 28, Appl
Sequence 582, App
Sequence 581, App
Sequence 1213, Ap
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Sequence 9, Appli
Sequence 11, Appl
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Sequence 26, Appl
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US-09-918-995-10122	US-09-754-853A-1	US-10-239-676-36	US-10-239-676-209	US-09-969-373-1212	US-09-960-352-368	US-09-969-373-739	US-10-239-676-93	US-10-239-676-96	US-10-239-676-67	US-10-196-063-1	US-10-239-676-188	us-09-737-178-119	US-09-737-178-109	US-09-790-988-1	US-09-790-988-1	US-09-960-352-6529	US-10-239-676-64	US-10-239-676-94	US-09-911-088-3	US-10-239-676-63	US-10-239-676-18	US-09-919-580-857	US-10-239-676-20	US-09-969-373-1172	US-10-104-580-9
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Sequence 10122, A	Sequence 1, Appli	Sequence 36, Appl	Sequence 209, App	Seguence 1212, Ap	Sequence 368, App	Sequence 739, App	Sequence 93, Appl	Sequence 96, Appl	Sequence 67, Appl	Sequence 1, Appli	Seguence 188, App	Seguence 119, App	Sequence 109, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 6529, Ap	Sequence 64, Appl	Sequence 94, Appl	-		Sequence 18, Appl	Sequence 857, App	Sequence 20, Appl	$\mathbf{-}$	Sequence 9, Appli

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/940,550A CURRENT FILING DATE: 2001-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: MCKERSIE, BRYAN
TITLE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 16313-0055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MANKIN, LUKE APPLICANT: MCKERSIE, BI
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181 ATAACTTTTCTAATATATATGACCAAAATTTGTTGATGTGCAGGTACGCGGGTGCTTACGAC
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                                                   AAAGAATGTAGTATATAGCAATTGCTTTTCTGTAGTTTATAAGTGTGTATATTTTAATTT
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SULT 2 -09-940-550 Publication GENERAL INFC APPLICANT: APPLICANT: TITLE OF IN FILE REFERE CURRENT APP CURRENT FILL PRIOR APPLI PRIOR APPLI PRIOR APPLI PRIOR APPLI PRIOR DI PRIOR PILL PRIO	1741 1801 1801 1861 1861 1861 1921 1921	1441 1501 1501 1561 1561 1561 1621 1621 1681 1681	1321 1321 1381 1381 1381
940-550A-9 940-550A-9 940-550A-9 940-550A-9 1cation No. US20030033635A1 IRAL INFORMATION: RAL INFORMATION: LICANT: MCKERSIE, BYAN LICANT: MCKERSIE, BYAN LE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF E REFERENCE: 16313-0055 E RENT APPLICATION NUMBER: US/09/940,550A RENT FILING DATE: 2001-08-27 OR APPLICATION NUMBER: 60/227,961 OR FILING DATE: 2000-08-25 BER OF SEQ ID NOS: 12 TWARE: Patentin Ver. 2.1 ID NO 9 NGTH: 2031 PE: DNA ATURE: NGTH: 2031 PE: DNA ATURE: BER INFORMATION: Description of Artificial Sequence: C31int DNA HER INFORMATION: sequence	98 92 9 8 6 6 9		

		1 CGCATGGACGCTGACGCCG	Db 96
	GCCGACCCGGGGCGAGACGATTGGGAAGAAGACCGCTTC	GCATGGACGCTGACGCCG	Оу 96
	AGCCGCCATTCACCCGGGCAGCATCACGGGGCTTTGTAAG 960	1 CCCTTCAAGCCGGGCAGTC	Db 90
	GCCGCCATTCACCCGGGCAGCATCACGGGGCTTTGTA	CCTTCAAGCCGGGCAGTC	Оу 90
		1 GAGTTCGAGCCCGACGTAATCC	84
	CGCTGGTGGCGTGAGATCAAGACGCACAAACACCT	AGTTCGAGCC	Оу 84
	CAACAAGTTAGCGCACTCGACCACTCCCCTTACCGGACCCTTC 840	1 ATGGTCAATGTCGTCATCA 	Qy 78 Db 78
	CTTGTTTCGGAGACGAAGGAGATCACGCGCAACGGCCG	GGCGCCTTACGGCTTC	
	GAGCTTGTTTCGGAGACGAAGGAGATCACGCGCAACGGCCGA 780	1 AAGGCGCCTTACGCCTTCG	
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	GAAGAACCTTCAGCGCGAATTGGGCGGGTACGTCGGCGG	CGGCGAAGATTCTCGAC	Оу 66
		ATGGACCTGATTCACCTGA	Db 60
	TATGCGGCTCGACGCGTCGCACAAAGAATCTTCGCTGAA	1 ATGGACCTGATTCACCTG	Оу 60
		1 CTCGCCCTGGGCGTGACGAT	54
	TGTTTCCACTCAGGAAGGCGTCTTCCGGCAGGGAAACG	TCGCCCTGGGCGTG	Qy 54
	4	1 GACGTGTCGCGCTTCTCGC	48
	CCTGAAGGTCATGGACGCGATTCCGGATTGTCTCGGAAT	ACGTGTCGCGCTT	0у 48
	NCGANTGCCGCGCCGGGCGGCTCAACATGATCATTGTCTAT 480	1 GAGTTCGAACGCATCCTGAA	Db 42
	CGAATGCCGCGCCGGCGGCTCAACATGATCATTGTCT	AGTTCGAACGCATC	Оу 42
		1 TTCGTCGGGCATTTCAGCG	Db 36
	CGCCGGGCACGTCGGCGTTCGGGACGGCGAGCGCCC	TCGTCGGGCATTTCAGC	Оу 36
		1 AACGAAGACAAGGCGGCCG	10b 30
	CCTTCAGCGCGAAGTCGAGCGCGACGGGGGGCCGGTTCAG	1 AACGAAGACAAGGCGGCC	Οу 30
	TCGAGCGCAGCAAGCCCAGCGACACAGCGTAGCGC	1 CGTCAGTCGCGCGAGCGCG	Db 24
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	ACGACGACGAAGACGACGCCCAGGACGGCACGGAAGACGTAGCGGCGTAG 203 	GGCAGGGAACGCCCATCGAGAAGCGCGCTTCGATCACGTGGGCGAAGCCGCCGACC 	CGCGTGTTCGTCGGGCTCTTCGTAGACAAGATCGTTGTCACGAAGTCGACTACGGGC 	ACGCCGACGCTGACCCGACCGGCCCTAAGTCGTGGTGGGGGGCGCGCGTCAGTAGACGAC 	CCGAA.		GCGGCAGGAGCTTACGACGGACCCGTTGGCAGG 	CGCCTGAGAAGAGCGGCGAACGGGCGAACCTTGTTGCGGAGCGCGCCGACGCCCTGAAC	ACGAAGAGACGTTGGCGCTTCTGTGGGAAGCCGCCGACGCTTCGGCAAGCTCACTGAG 	CGGCACTCGACAAGTTCGTTGCGGAACGCATCTTCAACAAGATCAGGCACGCCGAAGGC 	9TGGTCGACCCGTCCGCACCTGGGCAGCACGAAGGCACGTGCAACGTCAGCATG 	\TGACTTCGAAGCGCGGGGAAGAATCGATCAAGGACTCTTACCGCTGCCGTCGC 	GGCTTTCCCGGGGGCAAGCCATTCTGTCCGCCATGGACAAGCTGTÁCTGCGACAGTGTGGC 	CCGCTGAGTGGTATGAGCTTCAGGCGTGGTTGGACGGCAGGGGGCGCGCGC	ACCGCATTCAGCGCGACCCGATCACGCTCCGGCCGGTCGAGCTTGATTGCGGACCGATC	CCGCTGAGGTGATCTACAAGAAGAAGCCGGACGGCACCACGACCACGAAGATTGAGGGT 1 	GCGGGCTTC GCGGGCTTC

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OTHER INFORMATION: a, t, c, g

NAME/KEY: modified_base

LOCATION: (8478)

OTHER INFORMATION: a, t, c, g

NAME/KEY: modified_base

LOCATION: (8480)

OTHER INFORMATION: a, t, c, g

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APPLICANT: MANKIN, LUKE
APPLICANT: MAKENIE, BRYAN
APPLICANT: MCKERSIE, BRYAN
TITLE OF INVENTION: SELF-EXCISING POLYNUCLEOTIDES AND USES THEREOF
FILE REFERENCE: 16313-0055
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CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/227,961
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 11
SEQ ID NO 11
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NAME/KEY: modified_base
LOCATION: (1984)
OTHER INFORMATION: a, t, c, g, other or unknown
NAME/KEY: modified_base
LOCATION: (1986)
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CGTC-----AGTCGCGCGAGAGCGCGAGAATAGCAGTGCAGCAAGCCCAGCGACACAGCG
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                                                                                                        TAGCGCCAACGAAGACAAGGCCGCCGACCTTCAGCGCGAAGTCGAGCGCGACGGGGGCCCG 5343
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Qy	1074
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Qy	ω
Db	6364
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CURRENT APPLICATION NUMBER: US/09/788,297; CURRENT FILING DATE: 2001-02-16; NUMBER OF SEQ ID NOS: 34; SOETWARE: PatentIn Ver. 2.1; SEQ ID NO 20; LENGTH: 1842; TYPE: DNA; ORGANISM: Phage phiC31
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US-09-788-297-20
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APPLICANT: Calos, Michele P.
APPLICANT: Sclimenti, Christopher R.
TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
FILE REFERENCE: 8400-0011
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                       AGCAAGCCCAGCGACACACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA
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CGGGCGGCTCAACATGATCATTGTCTATGACGTGTCGCGCGTTCTCGCGCGCCTGAAGGTCAT
                                                                          GGTGGACACGTACGCGGGTGCTTACGACCGTCAGTCGCGCGAGGCGCGAAAATTCGAGCGC
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                                                  CTTCAACAAGATCAGGCACGCCGAAGGCGACGAAGAGAGACGTTGGCGCTTCTGTGGGAAGC
                                                                                                    GCACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCAT
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             CGCCCGACGCTTCGGCAAGCTCACTGAGGCGCCTGAGAAGAGCGGCGAACGGGCGAACCT
                                      CTTCAACAAGATCAGGCACGCCGAAGGCGACGAAGACGTTGGCGCTTCTGTGGGAAGC
                                                                                       GCACGAAGGCACGTGCAACGTCAGCATGGCGGCACTCGACAAGTTCGTTGCGGAACGCAT
                                                                                                                                        GATCAAGGACTCTTACCGCTGCCGTCGCCGGAAGGTGGTCGACCCGTCCGCACCTGGGCA
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CURRENT APPLICATION NUMBER: US/09/788,297
CURRENT FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 34
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 26
LENGTH: 1842
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence:altered; OTHER INFORMATION: recombinase 7C1
US-09-788-297-26
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US-09-788-297-26
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GENERAL INFORMATION:
APPLICANT: Calos, Michele P.
APPLICANT: Sclimenti ALITHICANTION:
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1801; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sclimenti, Christopher R.
TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
FILE REFERENCE: 8400-0011
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                                     AGTCGAGCGCGACGGGGCCCGGTTCAGGTTCGGCGCATTTCAGCGAAGCGCCGGCCAC
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273 AGCAAGCCCAGCGACACAGCGTAGCGCCAACGAAGACAAGGCGGCCGACCTTCAGCGCGA 332 	213 GATGTGCAGGTACGCGGGTGCTTACGACCGTCAGTCGCGCGAGAAATAGCAGTGC 272	Query Match 87.9%; Score 1785.6; DB 10; Length 1839; Best Local Similarity 99.0%; Pred. No. 0; Mismatches 1797; Conservative 0; Mismatches 19; Indels 0; Gaps 0;	FEATURE: OTHER INFORMATION: Description of Artificial Sequence:altered OTHER INFORMATION: recombinase 5C1 09-788-297-27	SEQ ID NO 27 LENGTH: 1839 TYPE: DNA ORGANISM: Artificial Sequence	CURRENT APPLICATION NUMBER: US/09/788,297 CURRENT FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 3401-02-16 SOFTWARE: Patentin Ver: 2.1	APPLICANT: Calos, Michele P. APPLICANT: Sclimenti, Christopher R. IITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION FILE REPERENCE: 8400-0011	US-09-788-297-27 : Sequence 27, Application US/09788297 : GENERAL TUFORMATION:	1824 GCAAGACGTAGCGGCGTAG 1842 JLT 6	1764 TTCGATCACGTGGGCGAAGCCGACCGACGACGACGACGACGACGCCCAGGACGCCACGGACGCCACGACG	TTCGATCACGTGGGCGAAGCCGCCGACGACGACGACGACGACGACGACGCCCAGGACGGCAC	1893 GATCGTTGTCACGAAGTCGACCTACGGGCAGGGGCAGGGGAACGCCCCATCGAGAAAGCGCGC 1952	1644 GTGGTGGGGGCGCGCGTCAGTAGACGACAAGCGCATGTTCGTCGGGCTCTTCGTAGACAA 1703	GCTTCCCCTTGACCAATGGTTCCCCGAAGACGCCGACGCTGACCCGACCGGCCCTAAGTC	1524 GCTCCGGCAGCAAGGGGCGGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA 1583 1773 GTTGCCCCTTGACCAATGGTTCCCCGAAGACGCCGACGGTGACCCGACCGGCCCTAAGTC 1832	1464 AGGCGCGTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACAGGCAGCGCTGAC 1523 1713 GCTCCGGCAGCAAGGGGCGGAAGAGCGGCTTGCCGAACTTGAAGCCGCCGAAGCCCCGAA 1772	AGGAGCTTACGACGGACCCGTTGGCAGGAAGCACTTCCGGAAGCAACACAGGCAGCACCGCTGAC	1593 TGTTGCGGAGCGCCGACGCCCTGAACGCCCTTGAAGAGCTGTACGAAGACCCGCGCGCC 1652	CGCCCGACGCTTCGGCAAGCTCACTGAGGCGCCTGAGAAGAGCGGCGGAACGGCGAACCT	
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CURRENT APPLICATION NUMBER: US/09/788,297
CURRENT FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 1833
TYPE: DNA
TYPE: DNA
ORGANISM: Artificial Sequence
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                                              Query Match
Best Local Similarity
Matches 1790; Conserv
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                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/09788297
Patent No. US20020094516A1
                                                                                                                                                                                                                                                                        APPLICANT: Sclimenti, Christopher R.
TITLE OF INVENTION: ALTERED RECOMBINASES FOR GENOME MODIFICATION
FILE REFERENCE: 8400-0011
                                                                                                                                                                                                                                                                                                    APPLICANT: Calos, Michele P. APPLICANT: Sclimenti, Chris
                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:altered OTHER INFORMATION: recombinase IC1
                                                                                                                                                   FEATURE:
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98.8%;
                                             Score 1767; Di
Pred. No. 0;
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      APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
PITTLE OF INVENTION: Promoters for regulation of FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
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                                                                                                                                                                                                                 Sequence 582, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION:
                                                                                                                                          APPLICANT: APPLICANT:
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Chang, H.
Zhu, T.
Han, B.
NOS:
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                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-581
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US-09-887-576-581
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APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Zhu, T.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
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SEQ ID NO 582
LENGTH: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
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Patent No. US20020144047A1
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                                                                                                                                                             Query Match
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PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of
FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
                                                                                                                                                                                                                     LENGTH: 11180
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nes 195; Conserv
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                                                                                                                                      9.6%; Score 195; DB 10; ilarity 100.0%; Pred. No. 4.7e-36; Conservative 0; Mismatches 0;
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; ORGANISM: Glycine max
US-09-969-373-1213
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US-09-969-373-1213/c
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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LENGTH: 248
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PRIOR FILING DATE: 2000-
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-
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                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                  APPLICANT:
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
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PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                       PPLICANT:
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ITTLE OF INVENTION: SOYbean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 ATAAATATGTTCTACTACTAATAAATAAATAATATAT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 TTTAATTTATAACTTTTCTAATATATGACCAAAATTT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 TCAAAATAAAAGAATGTAGTATATAGCAATTGCTTTTCTGTAGTTTATAAGTGTGTATAT 172
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                                           APPLICATION NUMBER: 60/
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FILING DATE: 2000-02-24
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                                  APPLICATION NUMBER:
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Parodi, الد.
اسط, Peter
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58.6%;
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60/184,822
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Pred. No. 0.0045;
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Db 11188 GTTTTTGCGTTTGTTTTAGTTGGATTTTTTTTTTTTATTAGTTAAAATGTTATTTTTA 11247
                                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-222
                                                                                                                                                                                : 2000-09-01
NUMBER OF SEQ ID N
: SEQ ID NO 222
LENGTH: 14708
: TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-791-279-27
                                                   Query Match
Best Local Similarity 57.8
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 222, Publication No
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Best Local Similarity 61.7
Matches 82: Conservative
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PRIOR FILING DATE: 2000-0
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 2000-0
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LENGTH: 740
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                 ORGANISM: Artificial Sequence
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TTLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
TLE REFERENCE: 5013.1003
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                  APPLICATION NUMBER:
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o. US20030082609A1
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                                                                          Score 50; DB 9
Pred. No. 0.27;
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Pred. No. 0.021;
""" tomatches 51;
                                                            Mismatches
                                                                                        DB 9;
                                                                                      Length 14708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID
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APPLICANT: RAO, ERCOLE
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                                                                                      LOCATION: (2880)
OTHER INFORMATION: a, c,
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LOCATION: (1498)..(1807)
OTHER INFORMATION: part
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LOCATION: (5305)..(5512)
OTHER INFORMATION: part
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LOCATION: (3844)...(4068)
OTHER INFORMATION: pET92
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LOCATION: (2665)
OTHER INFORMATION: a, c,
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LOCATION: (4545)..(4619)
OTHER INFORMATION: pET92
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LOCATION: (4326)..(4437)
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                 ME/KEY:
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                                                                              PRIOR APPLICATION NUMBER: PCT/EP01/03968
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                                                                                                CURRENT FILING DATE:
                                                                                                  CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                    APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene
FILE REFERENCE: 5013.1003
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Publication No. US20030059805A1
                   DE 10019058.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/EP97/05355
PRIOR FILING DATE: 1997-09-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GROWTH GENE AND SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: RAPPOLD-HOERBRAND, GUDRUN
APPLICANT: RAO, ERCOLE
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